

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:30:17 ; Search time 61 Seconds
(without alignments)
1426.633 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAEENLESLCTESNVNDE.....SACCFSPKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Jan04:*

- 1: geneseqp1980as:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1579	99.7	308	3 AAG47103	Aag47103 Arabidops
2	1573	99.4	308	2 AAY14071	Aay14071 Mitogenic
3	1565	98.9	308	3 AAG23337	Aag23337 Arabidops
4	1473	93.1	287	3 AAG47104	Aag47104 Arabidops
5	1459	92.2	287	3 AAG23338	Aag23338 Arabidops
6	1404	88.7	273	3 AAG47105	Aag47105 Arabidops
7	1390	87.8	273	3 AAG23339	Aag23339 Arabidops
8	627.5	39.6	358	7 ABR61588	Abt-61588 Z. mays c
9	621.5	39.3	358	3 AAY79321	Aay79321 Maize cyc
10	620.5	39.2	358	3 AAY79322	Aay79322 Maize cyc
11	554.5	35.0	390	3 AAY79323	Aay79323 Maize cyc
12	531.5	33.6	388	2 AAY31897	Aay31897 Corn cycl
13	443.5	28.0	328	3 AAG29789	Aag29789 Arabidops
14	443.5	28.0	339	3 AAG29788	Aag29788 Arabidops
15	441.5	27.9	320	3 AAG29790	Aag29790 Arabidops
16	416.5	26.3	339	2 AAY31894	Aay31894 Soybean c
17	402	25.4	318	2 AAY31895	Aay31895 Soybean c
18	362.5	22.9	367	3 AAG23946	Aag23946 Arabidops
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20	353	22.3	361	3 AAG07075	Aag07075 Arabidops
21	349	22.0	307	3 AAG23947	Aag23947 Arabidops
22	343.5	21.7	308	3 AAG07076	Aag07076 Arabidops
23	343.5	21.7	308	3 AAG53865	Aag53865 Arabidops
24	301.5	19.0	359	5 AAY75636	Aay75636 M. Truncu
25	294.5	18.6	238	2 AAY31892	Aay31892 Corn cycl

ALIGNMENTS

RESULT 1
AAG47103

ID AAG47103 standard; protein; 308 AA.

XX AAG47103;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 59333.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

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Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAEENLESLCTESNVDDGMIVDTPETPIEISIPQMGFSQSESEIIMEMVKEKQHLPS 60
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DB 61 DDYIKRLRSGDLDLVNRRDALNWIWKAQEVHGFGLCFCLAMNYLDRLFSVHDLPSGKG 120
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DB 121 WILQLAVACLALSLAAKIEETEVEPMLIDLVQGDQPFVFEAKSVORMELLVNLKWLRLAI 180
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DB 181 TPCSYIRYFLRKMSKCDQPSNTLISRSLOVIASTTKGIDFLFRPSEAAAAVALSVSGE 240
QY 241 LQRVHFDNSSFSLFLSLQKERVKKIGEMIESDGLCSQTPNGVLEVSACCFSPKTHDS 300
DB 241 LQRVHFDNSSFSLFLSLQKERVKKIGEMIESDGLCSQTPNGVLEVSACCFSPKTHDS 300
QY 301 SSSYTHLS 308
DB 301 SSSYTHLS 308

RESULT 2
AA14071
ID AA14071 standard; protein; 308 AA.
XX AA14071;
XX
XX 16-JUL-1999 (first entry)
XX
XX Mitogenic cyclin CYCD4 protein sequence.
XX
XX Mitogenic cyclin; CYCD4; modulator; plant cell cycle; growth inhibitor;
XX plant cell division; cell growth; regulator; cell proliferation;
XX growth regulator; herbicide; cell division progression.
XX
XX Arabidopsis thaliana.
XX
XX WO9922002-A1.
XX
XX 06-MAY-1999.
XX
XX 23-OCT-1998; 98WO-EP006749.
XX
XX 24-OCT-1997; 97EP-00203303.
XX
XX (CROP-) CROPDISEIGN NV.
XX
XX Inze D, De Veylder L, De Almeida J;
XX
XX WPI; 1999-312966/26.
XX
XX N-PSDB; AAX36897.
XX
XX DNA sequence encoding a mitogenic cyclin.
XX
XX Claim 1; Page 47-49; 57pp; English.
XX

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CC This sequence is the mitogenic cyclin, CYCD4, of the invention. The DNA
CC sequence, vectors containing it, protein encoded by it, or antibodies
CC recognising the protein can be used for modulating plant cell cycle,
CC plant cell division and/or growth, for influencing the activity of
CC mitogenic cyclin in a plant cell, as positive or negative regulator of
CC cell proliferation, for modifying the growth inhibition caused by
CC environmental stress conditions, or for use in a screening method for the
CC identification of inhibitors or activators of cell cycle proteins. A
CC compound which is an activator or inhibitor of the mitogenic cyclin can
CC be used as a growth regulator and/or herbicide. The proteins can also be
CC used to influence cell division progression in yeast, mammals and insects
XX
XX Sequence 308 AA;
XX
Query Match 99.4%; Score 1573; DB 2; Length 308;
Best Local Similarity 99.7%; Pred. No. 2.4e-165;
Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MAEENLESLCTESNVDDGMIVDTPETPIEISIPQMGFSQSESEIIMEMVKEKQHLPS 60
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RESULT 3
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XX AAG23337;
XX
XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 26608.
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XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX Arabidopsis thaliana.
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XX EP1033405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-00301439.
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Db	61	DDYIKRLSGDLNNGRRDALNWKACEVHQFGPLCFCLAMNYLDRFLSVHDLPSGKG 120			
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Qy	241	LQRVHFNSSPFLSFLSLQKERVKKIGEMIESDGLSCQTPNGVLEVSACCFKTHDS 300			
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Qy	301	SSSYTHLS 308			
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KW	KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KW	KW	termination sequence.			
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OS	OS	Arabidopsis thaliana.			
XX	XX				
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Best Local Similarity 99.7%; Pred. NO. 2.6e-154;

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RESULT 5

AAG23338

ID AAG23338 standard; protein; 287 AA.

XX AAG23338;

XX 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 26609.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EP1033405-A2.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 92.2%; Score 1459; DB 3; Length 287;
Best Local Similarity 99.0%; Pred. No. 9,4e-153;
Matches 284; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 22 MIVDETPIIISIPQMGFSQSESEIIMWVEKEKQHLPSDDYIKRLRSGDLINVGRRDA 81
Db 1 MIVDETPIIISIPQMGFSQSESEIIMWVEKEKQHLPSDDYIKRLRSGDLINVGRRDA 60
QY 82 LNWIKACEVHQFGPICFCLAMNYLDRFLSPGKGMILQLAVACLSAAKTEETE 141
Db 61 LNWIKACEVHQFGPICFCLAMNYLDRFLSPGKGMILQLAVACLSAAKTEETE 120
QY 142 VPMILDLQVGDPOVFPEAKSVQRMELLVNLKWLRLRAITPCSYIRYFLKMSKCDQEPS 201
Db 121 VPMILDLQVGDPOVFPEAKSVQRMELLVNLKWLRLRAITPCSYIRYFLKMSKCDQEPS 180
QY 202 NTLISRLQVIASITTKGIDFLFRPSEAAAVALSVGELQRVHFNSSPFLSLLOKE 261
Db 181 NTLISRLQVIASITTKGIDFLFRPSEAAAVALSVGELQRVHFNSSPFLSLLOKE 240
QY 262 RVKIGIMIESDGLSCQTPNGVLEVSACCFGFKTHDSSSYTHLS 308
Db 241 RVKIGIMIESDGLSCQTPNGVLEVSACCFGFKTHDSSSYTHLS 287
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RESULT 6
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XX AAG47105;
AC AAG47105;
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 59335.
XX Arabidopsis thaliana.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX Arabidopsis thaliana.
PN EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
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Query Match 88.7%; Score 1404; DB 3; Length 273;
Best Local Similarity 99.6%; Pred. No. 1.1e-146;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MGFQSESEEEIIMENVEKEKQHLPSDDYIKRLRSGDLNLNVRDRLNWKACEVHQFG 60
QY 96 PLCFCFLANNYLDRFLSVHDLPSGKGWILQLLAVACLISAAKIEETEVPMLIDLQVGDPOF 155
DB 61 PLCFCFLANNYLDRFLSVHDLPSGKGWILQLLAVACLISAAKIEETEVPMLIDLQVGDPOF 120
QY 156 VFEAKSVQRMELLVNLKLNKRLRAITPCSYIRYFLRKMCKDQEPSNTLISRSLQVIAS 215
DB 121 VFEAKSVQRMELLVNLKLNKRLRAITPCSYIRYFLRKMCKDQEPSNTLISRSLQVIAS 180
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OY 216 TKGIDFLERPERSEAAANVALSVSGELORVHFDNSSFPLSLLOKERVKKIGEMIESDGS 275
181 TKGIDFLERPERSEAAANVALSVSGELORVHFDNSSFPLSLLOKERVKKIGEMIESDGS 240
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Db 241 DLCSOTPNGVLEVSACCFKTHDSSSYTHLS 273

RESULT 7
AAG23339
ID AAG23339 standard; protein; 273 AA.
XX
AC AAG23339;
DT
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26610.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
PF
PF 25-FEB-2000; 2000EP-00301439.
XX
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PR 28-APR-1999; 99US-0131449P.
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Query Match 87.8%; Score 1390; DB 3; Length 273;
Best Local Similarity 98.9%; Pred. No. 3.9e-145;
Matches 270; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 12 LLCAEDNAALGLDDDDGESSWAAATPPRTVAAAATGVAVDGLTTEFPL----- 63
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 QY 96 PLCFCIAMNYLDRFLPSGKHWILOLAVACLSLAAKTEETVPMILDLQVGDPOF 155
 DB 120 PLTAVLSVNYLDRFLSTYEFPEGRAMWTQLLAVACLSLASKIEETFPVPLDLQVAEAKF 179
 QY 156 VFEAKSVQRMELVLNKLKWLRAITPCSYIRYFLRKMCKDQEPSNTLISRLQVIAS 215
 DB 180 VEGRIKKNMELVLSTLKWRAHVATCSFVEFLHKLSD-HGAPSLARSRLDLVST 238
 QY 216 TKGIDFLFRPSEAAVALSVSGELQRVHFDNSSFPLSLQKERVKKIGEMIE---- 271
 DB 239 AKGAFFVFRPSEIAASVALAIGECRSSVIERAASSCKY--LDKERVLCHEMIQEKIT 296
 QY 272 -----SDGSLCS--QTPNGVLEVSAC-----CFSFKTHDSSSS 303
 DB 297 AGSIVLKSGSSISSVPSQPIGVLDAAACLSQQSDDATVGSAPVCY----HSSSTS 348
 RESULT 9
 AAY79321
 ID AAY79321 standard; protein; 358 AA.
 XX
 AC AAY79321;
 XX
 DT 18-JUL-2000 (first entry)
 XX
 DE Maize cyclin D.
 XX
 KW Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
 KW transgenic plant.
 XX
 OS Zea mays.
 XX
 PN WO200017364-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 21-SEP-1999; 99WO-US021946.
 XX
 PR 23-SEP-1998; 98US-0101551P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, Mcclver JA;
 PI Hoerster GJ;
 XX
 XX WPI; 2000-283589/24.
 DR N-PSDB; AA294581.
 XX
 PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
 PT related proteins and antisense RNA useful for control of cell cycle
 PT regulation.
 XX
 PS Claim 16; Page 117-118; 134pp; English.

The present sequence is that of an isoform of maize cyclin D (CycD), a protein necessary for progression from G1 into S phase. CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression

CC of the polynucleotide sufficient to modulate (increase or decrease) the
 CC CycD protein in the cell. The CycD protein is present in an amount
 CC sufficient to alter cell division, increase the number of cells dividing,
 CC improve transformation frequencies, alter cell growth, increase the
 CC growth rate, increase crop yield, alter plant height or size, enhance or
 CC inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen)
 CC growth, produce organ ablation, produce parthenocarpic fruits, produce
 CC male sterile plants, enhance embryogenic response, increase callus
 CC induction, provide positive selection, increase plant regeneration, alter
 CC the time that cells are arrested in G1 or G0 phase or in a particular
 CC cell cycle, improve response to environmental stress including
 CC dehydration, heat or cold, increase the number of pods per plant,
 CC development, provide hormone-independent cell growth, or increase the
 CC growth rate of cells in bioreactors. The level of CycD protein in the
 CC cells is transiently modulated by introducing CycD RNA or CycD
 CC polypeptides. All claimed
 XX
 SQ Sequence 358 AA;

Query Match 39.3%; Score 621.5; DB 3; Length 358;
 Best Local Similarity 39.9%; Pred. No. 1e-59;
 Matches 142; Conservative 59; Mismatches 74; Indels 81; Gaps 10;
 QY 10 LLCTESN-----VDDSGM-----IVDETPTIEISIPQMG 37
 DB 12 LLCAEDNAAILGLDDDDGEESWAAATPPRTVAAAAATGAVDGLITFPD----- 63
 QY 38 FQSESEIEMVEKEKQHLPSDDYIKRL--RSGDLINVGRRDALNWIWACEVHQFG 95
 DB 64 ----LSDDCVATLVEKEVEHMPAEGYLOKQRRHGDLDAAVRKDAIDWIKVIEHYNEA 119
 QY 96 PLCFCIAMNYLDRFLPSGKHWILOLAVACLSLAAKTEETVPMILDLQVGDPOF 155
 DB 120 PLTAVLSVNYLDRFLSTYEFPEGRAMWTQLLAVACLSLASKIEETFPVPLDLQVAEAKF 179
 QY 156 VFEAKSVQRMELVLNKLKWLRAITPCSYIRYFLRKMCKDQEPSNTLISRLQVIAS 215
 DB 180 VEGRIKKNMELVLSTLKWRAHVATCSFVEFLHKLSD-HGAPSLARSRLDLVST 238
 QY 216 TKGIDFLFRPSEAAVALSVSGELQRVHFDNSSFPLSLQKERVKKIGEMIE---- 271
 DB 239 AKGAFFVFRPSEIAASVALAIGECRSSVIERAASSCKY--LDKERVLCHEMIQEKIT 296
 QY 272 -----SDGSLCS--QTPNGVLEVSAC-----CFSFKTHDSSSS 303
 DB 297 AGSIVLKSGSSISSVPSQPIGVLDAAACLSQQSDDATVGSAPVCY----HSSSTS 348

RESULT 10
 AAY79322
 ID AAY79322 standard; protein; 358 AA.

XX
 AC AAY79322;
 XX
 DT 18-JUL-2000 (first entry)
 XX
 DE Maize cyclin D.
 XX
 KW Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
 KW transgenic plant.
 XX
 OS Zea mays.
 XX
 PN WO200017364-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 21-SEP-1999; 99WO-US021946.
 XX
 PR 23-SEP-1998; 98US-0101551P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.

XX PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, Mcelver JA;
 PI Hoerster GU;
 XX DR WPI; 2000-283589/24.
 XX DR N-PSDB; AA294582.
 XX PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
 PT related proteins and antisense RNA useful for control of cell cycle
 PT regulation.
 XX PS Claim 16; Page 121-122; 134pp; English.
 XX CC The present sequence is that of an isoform of maize cyclin D (CycD), a
 CC protein necessary for progression from G1 into S phase. CycD binds to
 CC CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma
 CC associated protein, releasing the E2F transcription factor which
 CC activates DNA synthesis. The invention provides maize CycD
 CC polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that
 CC are involved in cell cycle regulation. Also provided are recombinant
 CC expression cassettes (including ZmCycD in sense or antisense
 CC orientation), host cells, transgenic plants (especially corn, sorghum,
 CC sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and
 CC antibody compositions. A claimed method of modulating the level of CycD
 CC protein in a cell comprises transforming the cell with a recombinant
 CC expression cassette comprising a CycD polynucleotide linked to a
 CC promoter, and growing the cell for a time sufficient to induce expression
 CC of the polynucleotide sufficient to modulate (increase or decrease) the
 CC CycD protein in the cell. The CycD protein is present in an amount
 CC sufficient to alter cell division, increase the number of cells dividing,
 CC improve transformation frequencies, alter cell growth, increase the
 CC growth rate, increase crop yield, alter plant height or size, enhance or
 CC inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen)
 CC growth, produce organ ablation, produce parthenocarpic fruits, produce
 CC male sterile plants, enhance embryogenic response, increase callus
 CC induction, provide positive selection, increase plant regeneration, alter
 CC the time that cells are arrested in G1 or G0 phase or in a particular
 CC cell cycle, improve response to environmental stresses including
 CC dehydration, heat or cold, increase the number of pods per plant,
 CC increase the number of seeds per pod or ear, alter the lag time in seed
 CC development, provide hormone-independent cell growth, or increase the
 CC growth rate of cells in bioreactors. The level of CycD protein in the
 CC cells is transiently modulated by introducing CycD RNA or CycD
 CC polypeptides. All claimed
 XX SQ Sequence 358 AA;

Query Match 39.2%; Score 620.5; DB 3; Length 358;
 Best Local Similarity 39.9%; Pred. No. 1.3e-59;
 Matches 142; Conservative 59; Mismatches 74; Indels 81; Gaps 10;

QY 10 LLCTESN-----VDDEGM-----IVDETPTEISIPQM 37
 DB 12 LLCAEDNAAILGLDDGESSWAAATPPRTVAAAATGVAVDGILTFEP- 63
 QY 38 FQOSESEIIMBEWEKEQHLPSDDYIKRL--RSGDLNLCVGRDALNWKACEVHFG 95
 DB 64 ----LSDDCVATLVEKEVHEMPAEGYQLQRHGDLDLVAVKQADINWKVIEHNP 119
 QY 96 PLCFCLAMNYLDRFLSVHDLPSPGKGMILQLLAVACLAAKIEETEVEPMLDQVDPQF 155
 DB 120 PLTAVLSVNYLDRFLSTVEFPEGRAWMTQLLAVACLSLAKIEETFPVPLDQVAEAKF 179
 QY 156 VPEAKSVQRMELLVLNKLWRLRAITPCSYIRYFLKMSKCDQPSNTLISRSLQVIAT 215
 DB 180 VFEGRITKMEMLLVLTSLKWRHVAFTACSFVEYFLHLKLSL-HGAPSLARSRSLLVLT 238
 QY 216 TKGIDFLFPRPEAAVAALSVSGELQRVHFNPSFSLFSLQKERVKKIGEMTE---- 271
 DB 239 AKGAEFVFRPEELAAVALAIGECRSSVIERAASSCKY--LDKERVLRCHEMIQEKIT 296
 QY 272 -----SDGSLCS--QTPNGVLEVSAC-----CFSEKTHDSSSS 303

DB 237 MGSIVLKSAGSSISSVPOSPIGVLDAAACLSQQSDDATVGSFVACY-----HSSSTS 348

RESULT 11
 AAY79323
 ID AAY79323 standard; protein; 390 AA.
 XX AC AAY79323;
 XX DT 18-JUL-2000 (first entry)
 XX DE Maize cyclin D.
 XX KW Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
 KW transgenic plant.
 XX OS Zea mays.
 XX PN WO200017364-A2.
 XX PD 30-MAR-2000.
 XX PF 21-SEP-1999; 99WO-US021946.
 XX PR 23-SEP-1998; 98US-0101551P.
 XX PA (PION-) PIONEER HI-BRED INT INC.
 XX PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, Mcelver JA;
 PI Hoerster GU;
 XX WPI; 2000-283589/24.
 DR N-PSDB; AA294583.
 XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
 PT related proteins and antisense RNA useful for control of cell cycle
 PT regulation.
 XX PS Claim 16; Page 124-125; 134pp; English.
 XX CC The present sequence is that of an isoform of maize cyclin D (CycD), a
 CC protein necessary for progression from G1 into S phase. CycD binds to
 CC CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma
 CC associated protein, releasing the E2F transcription factor which
 CC activates DNA synthesis. The invention provides maize CycD
 CC polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that
 CC are involved in cell cycle regulation. Also provided are recombinant
 CC expression cassettes (including ZmCycD in sense or antisense
 CC orientation), host cells, transgenic plants (especially corn, sorghum,
 CC sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and
 CC antibody compositions. A claimed method of modulating the level of CycD
 CC protein in a cell comprises transforming the cell with a recombinant
 CC expression cassette comprising a CycD polynucleotide linked to a
 CC promoter, and growing the cell for a time sufficient to induce expression
 CC of the polynucleotide sufficient to modulate (increase or decrease) the
 CC CycD protein in the cell. The CycD protein is present in an amount
 CC sufficient to alter cell division, increase the number of cells dividing,
 CC improve transformation frequencies, alter cell growth, increase the
 CC growth rate, increase crop yield, alter plant height or size, enhance or
 CC inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen)
 CC growth, produce organ ablation, produce parthenocarpic fruits, produce
 CC male sterile plants, enhance embryogenic response, increase callus
 CC induction, provide positive selection, increase plant regeneration, alter
 CC the time that cells are arrested in G1 or G0 phase or in a particular
 CC cell cycle, improve response to environmental stresses including
 CC dehydration, heat or cold, increase the number of pods per plant,
 CC increase the number of seeds per pod or ear, alter the lag time in seed
 CC development, provide hormone-independent cell growth, or increase the
 CC growth rate of cells in bioreactors. The level of CycD protein in the
 CC cells is transiently modulated by introducing CycD RNA or CycD
 CC polypeptides. All claimed
 XX SQ Sequence 390 AA;

RESULT 13	
AAG29789	
ID	AAG29789 standard; protein; 328 AA.
XX	
AC	AAG29789;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 35502.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
EW	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
XX	
PR	25-FEB-1999; 99US-0121825P.
PR	05-MAR-1999; 99US-0123180P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127462P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0129845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	23-APR-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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PR 14-MAY-1999; 99US-0134219P.
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PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 18-JUN-1999; 99US-0139750P.
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PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
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PR 19-JUL-1999; 99US-0144332P.
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PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 23-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
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PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
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PR 18-AUG-1999; 99US-0149426P.
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PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150804P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151438P.
PR 07-SEP-1999; 99US-0151930P.
PR 10-SEP-1999; 99US-0152363P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
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PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.

XX	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KX	termination sequence.
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
PD	
XX	
PF	06-SEP-2000.
XX	
PP	25-FEB-2000; 2000EP-00301439.
XX	
PR	25-FEB-1999; 99US-0121825P.
PR	05-MAR-1999; 99US-0123380P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127462P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0129845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	23-APR-1999; 99US-0130891P.
PR	28-APR-1999; 99US-0131449P.
PR	30-APR-1999; 99US-0132048P.
PR	30-APR-1999; 99US-0132407P.
PR	04-MAY-1999; 99US-0132484P.
PR	05-MAY-1999; 99US-0132485P.
PR	06-MAY-1999; 99US-0132486P.
PR	07-MAY-1999; 99US-0132487P.
PR	11-MAY-1999; 99US-0132863P.
PR	14-MAY-1999; 99US-0134255P.
PR	14-MAY-1999; 99US-0134218P.
PR	14-MAY-1999; 99US-0134219P.
PR	14-MAY-1999; 99US-0134370P.
PR	18-MAY-1999; 99US-0134768P.
PR	19-MAY-1999; 99US-0134941P.
PR	20-MAY-1999; 99US-0135124P.
PR	21-MAY-1999; 99US-0135353P.
PR	24-MAY-1999; 99US-0135629P.
PR	25-MAY-1999; 99US-0136021P.
PR	27-MAY-1999; 99US-0136332P.
PR	28-MAY-1999; 99US-0136782P.
PR	01-JUN-1999; 99US-0137222P.
PR	03-JUN-1999; 99US-0137528P.
PR	04-JUN-1999; 99US-0137502P.
PR	07-JUN-1999; 99US-0137724P.
PR	08-JUN-1999; 99US-0138094P.
PR	10-JUN-1999; 99US-0138540P.
PR	14-JUN-1999; 99US-0138847P.
PR	16-JUN-1999; 99US-0139119P.
PR	16-JUN-1999; 99US-0139452P.
PR	17-JUN-1999; 99US-0139453P.
PR	18-JUN-1999; 99US-0139459P.
PR	18-JUN-1999; 99US-0139460P.
PR	18-JUN-1999; 99US-0139461P.
PR	18-JUN-1999; 99US-0139462P.
PR	18-JUN-1999; 99US-0139463P.
PR	18-JUN-1999; 99US-0139750P.
PR	18-JUN-1999; 99US-0139763P.
PR	21-JUN-1999; 99US-0139817P.
PR	22-JUN-1999; 99US-0139899P.
PR	23-JUN-1999; 99US-0140055P.
PR	23-JUN-1999; 99US-0140354P.
PR	24-JUN-1999; 99US-0140695P.
PR	28-JUN-1999; 99US-0140823P.
PR	29-JUN-1999; 99US-0140991P.
PR	30-JUN-1999; 99US-0141287P.
PR	01-JUL-1999; 99US-0141842P.
PR	01-JUL-1999; 99US-0142154P.
PR	02-JUL-1999; 99US-0142055P.
PR	06-JUL-1999; 99US-0142390P.
PR	08-JUL-1999; 99US-0142803P.
PR	09-JUL-1999; 99US-0142920P.
PR	12-JUL-1999; 99US-0142977P.
PR	13-JUL-1999; 99US-0143542P.
PR	14-JUL-1999; 99US-0143624P.
PR	15-JUL-1999; 99US-0144005P.
PR	16-JUL-1999; 99US-0144085P.
PR	16-JUL-1999; 99US-0144086P.
PR	19-JUL-1999; 99US-0144325P.
PR	19-JUL-1999; 99US-0144331P.
PR	19-JUL-1999; 99US-0144332P.
PR	19-JUL-1999; 99US-0144333P.
PR	19-JUL-1999; 99US-0144334P.
PR	19-JUL-1999; 99US-0144335P.
PR	20-JUL-1999; 99US-0144352P.
PR	20-JUL-1999; 99US-0144632P.
PR	20-JUL-1999; 99US-0144884P.
PR	21-JUL-1999; 99US-0144814P.
PR	21-JUL-1999; 99US-0145086P.
PR	21-JUL-1999; 99US-0145088P.
PR	22-JUL-1999; 99US-0145085P.
PR	22-JUL-1999; 99US-0145087P.
PR	22-JUL-1999; 99US-0145089P.
PR	22-JUL-1999; 99US-0145192P.
PR	23-JUL-1999; 99US-0145145P.
PR	23-JUL-1999; 99US-0145218P.
PR	23-JUL-1999; 99US-0145224P.
PR	26-JUL-1999; 99US-0145276P.
PR	27-JUL-1999; 99US-0145913P.
PR	27-JUL-1999; 99US-0145918P.
PR	27-JUL-1999; 99US-0145919P.
PR	28-JUL-1999; 99US-0145951P.
PR	02-AUG-1999; 99US-0146386P.
PR	02-AUG-1999; 99US-0146388P.
PR	02-AUG-1999; 99US-0146389P.
PR	03-AUG-1999; 99US-0147038P.
PR	03-AUG-1999; 99US-0147204P.
PR	04-AUG-1999; 99US-0147302P.
PR	05-AUG-1999; 99US-01471

Query Match	27.9%	Score	441.5	DB	3	Length	320
Best Local Similarity	37.1%	Pred. No.	8e+40				
Matches	117	Conservative	52	Mismatches	105	Indels	41
Gaps	11						

Qy	8	LSLICTSNVDGMI	VDTEPIEISIPQMGFSQSESE---	EIIMVMEKEQHQLPSDDY	63
Db	1	MDLFCGE-----	DSGVFSGESTVD-----	FSSEVDSWPGDSIACFI	EDERHHVPGHDY 49
Qy	64	IKRLRSGDLNLNV	RRDALNIWKACEVHQFGPLCFCL	ANNYLDRFLSVHDLPSGKGWIL	123
Db	50	LSRFQTRSLDAS-	AREDSVAMILKVQAYNFCPLTAYL	AVNMDRFLYARELPETSCGWM	108
Qy	124	QLLAVACLSLAAK	TEETVPMILDLQVGDPQVFPEAKS	VQRMELLVNKLKWRRLAIPTC	183
Db	109	QLLAVACLSLAAK	MEIIVPSLFDQVQAGVKYLF	FEAKTIKGMELIIVLSVLDWRLSRV	VPFF 168
Qy	184	SYIRYFLRKMCKD	OEPNST---	LIRSLOVIASTTKGIDFLER	PSEAAAVALSVSG 239
Db	169	DFISGFAYKI-----	DPGSGTFLGFFISHATEIILSN	IKESAFLEYWPSISAAALCVAN	223
Qy	240	ELQRVHFNDSG	SPSLFSL-----	LQKRVVKIGEMIES---	DGSDLCSQTPNGV -LEV 288
Db	224	ELPSI---	SSVNVPHESPETWCDGLSK	EKIVRCYFLMKAMAIENNRL-	NTEKVIKLRV 278
Qy	289	SACCFSPKTHD	SSSS 303		

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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:36:26 ; Search time 23 Seconds
(without alignments)
691.339 Million cell updates/sec

Title: US-09-530-209A-2
Perfect score: 1583
Sequence: 1 MAEENLESLCTESNVDE.....SACCFSPKTHDSSSSYTHLS 308

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	722.5	45.6	354	US-09-404-296B-2	Sequence 2, Appli
2	635.5	40.1	361	US-09-404-296B-30	Sequence 30, Appl
3	621.5	39.3	358	US-09-398-858-2	Sequence 2, Appli
4	620.5	39.2	358	US-09-398-858-12	Sequence 12, Appl
5	554.5	35.0	390	US-09-398-858-14	Sequence 14, Appl
6	443.5	28.0	335	US-09-404-296B-28	Sequence 28, Appl
7	440.5	27.8	315	US-09-404-296B-8	Sequence 8, Appli
8	398	25.1	376	US-09-404-296B-32	Sequence 32, Appl
9	379	23.9	373	US-09-404-296B-4	Sequence 4, Appli
10	370.5	23.4	367	US-09-404-296B-6	Sequence 6, Appli
11	357.5	22.6	357	US-09-404-296B-10	Sequence 10, Appl
12	291.5	18.4	349	US-09-398-858-22	Sequence 22, Appl
13	239.5	15.1	660	US-08-770-761A-2	Sequence 2, Appli
14	237	15.0	295	US-08-464-517-20	Sequence 20, Appl
15	237	15.0	295	US-08-464-517-20	Sequence 20, Appl
16	237	15.0	295	US-08-463-772-20	Sequence 20, Appl
17	237	15.0	295	PCT-US93-05000-20	Sequence 20, Appl
18	237	15.0	309	US-08-464-517-4	Sequence 4, Appli
19	237	15.0	309	US-08-463-772-4	Sequence 4, Appli
20	236	14.9	295	US-07-947-120-8	Sequence 8, Appli
21	236	14.9	295	US-08-472-893A-8	Sequence 8, Appli
22	236	14.9	295	US-08-460-694-2	Sequence 2, Appli
23	236	14.9	295	US-08-460-744-2	Sequence 2, Appli
24	236	14.9	295	US-07-667-711B-2	Sequence 2, Appli
25	236	14.9	295	US-08-947-492-8	Sequence 8, Appli
26	236	14.9	618	US-08-770-761A-3	Sequence 3, Appli
27	236	14.9	647	US-08-770-761A-8	Sequence 8, Appli

28	236	14.9	662	2	US-08-770-761A-5	Sequence 5, Appli
29	236	14.9	705	2	US-08-770-761A-7	Sequence 7, Appli
30	234	14.8	295	2	US-08-464-517-2	Sequence 19, Appl
31	234	14.8	295	2	US-08-464-517-19	Sequence 19, Appl
32	234	14.8	295	2	US-08-246-361A-2	Sequence 2, Appli
33	234	14.8	295	2	US-08-246-361A-19	Sequence 19, Appl
34	234	14.8	295	3	US-08-463-772-2	Sequence 2, Appli
35	234	14.8	295	3	US-08-463-772-19	Sequence 19, Appl
36	234	14.8	295	5	PCT-US93-05000-2	Sequence 2, Appli
37	234	14.8	295	5	PCT-US93-05000-19	Sequence 19, Appl
38	232	14.7	289	2	US-08-246-361A-4	Sequence 4, Appli
39	232	14.7	289	5	PCT-US93-05000-4	Sequence 4, Appli
40	213.5	13.5	152	2	US-08-460-694-4	Sequence 4, Appli
41	213.5	13.5	152	3	US-08-460-744-4	Sequence 4, Appli
42	213.5	13.5	152	3	US-07-667-711B-4	Sequence 4, Appli
43	211	13.3	236	2	US-08-464-517-22	Sequence 22, Appl
44	211	13.3	236	2	US-08-246-361A-22	Sequence 22, Appl
45	211	13.3	236	3	US-08-463-772-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-404-296B-2
; Sequence 2, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-404-296B-2

Query Match 45.6%; Score 722.5; DB 4; Length 354;
Best Local Similarity 48.1%; Pred. No. 5.5e-75;
Matches 164; Conservative 60; Mismatches 76; Indels 41; Gaps 10;

QY	1	MAEENL----	ELSLCTESNV----	DDEGMIVDETPIEISIPQMGSQ-----	S 41
Db	1	MAADNIYDFVASNLLCTETKSLCFDDVDLSLTISQOINIEKSKDLSFNNIRSEPLIDLPS	60		
QY	42	ESEELIMEVKEKOHLPDDDYIKLRSGDLDLVNRRDALNMIWKACEVHGFGLCFCL	101		
Db	61	LSEECLSFVQKEMFLPKDDIVERLRSGDLDLSV-RKALDWILKAMHYGFGLSFLC	119		
QY	102	ANNYLDRFLSHVHDLPSGKGMIIQLLAVACLSLAAKIEETEVPMLIDLQVDPQFVPEAKS	161		
Db	120	SINYLDRFLSLVELPRSKTWTVQLLAVACLSLAAKMEENVPLTVDLQVDPKFFVEGKT	179		
QY	162	VORMELLVUNKWLRRAITPCSYTRYFLRKMCKDOEPSNTLISRLQVIATSTKGDIF	221		
Db	180	IORMELLVLTSLKWRMQAYTPYTFIDYFMKXNG-DQIFSRFLISGMOLLISIRSIDF	238		
QY	222	LEFRPSEAAAVALSVSGLQVRHFDNSFSFLSL-LQKERVKKIGEMIE-----	271		
Db	239	LEFRPSEIAASVAMSUSGIEIQAKDIDKA--MPCFFIHLDKGVQKVELIQDLTATIT	296		
QY	272	SDGSDICSQTPNGVLEVSACCFSKTHD-----	SSSYT 305		
Db	297	AAAASLVPSPIGVLE-AAACLSYKSGDERTVGSCTTSSHT	336		

RESULT 2
US-09-404-296B-30
; Sequence 30, Application US/09404296B

Db 239 AKGAEVFRSEIAASVALAAGECRSSVIERAASSCKY--LKERVLRCHEMIOEKIT 296
Qy 272 -----SDGDLCS--QTPNGVLEVSAC-----CFSFKTHDSSSS 303
Db 297 MGSIVLKSAGSISISVPQSPIGVLDAAACLSQSQSDDATVGSFAVCY----HSSSTS 348

RESULT 5

US-09-398-858-14
; Sequence 14, Application US/09398858
; Patent No. 6518487
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: 0926
; CURRENT APPLICATION NUMBER: US/09/398.858
; CURRENT FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 60/101.551
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Zea mays
US-09-398-858-14

Query Match 35.0%; Score 554.5; DB 4; Length 390;
Best Local Similarity 39.1%; Pred. No. 1.9e-55;
Matches 135; Conservative 52; Mismatches 89; Indels 69; Gaps 9;

Qy 10 LLCTESNVD---DEGMIVDETPIEISIPQMGFSQS-----ESEEIMEMVEK 53
Db 13 LLCAEHSIIWYDE---ESEELEAVGRRGRSGYGGDFGADLFPQSEECVAGLVER 68
Qy 54 EKQHLPSDDYIKRLSRGDLNVRDNLNWKACEVHQFGLCFCLAMNYLDRFLSVH 113
Db 69 ERDEWPGCYDLRLGGGCLCV--REAVDNIWKAYTHRRPLTAYLVNDRFLSLS 127
Qy 114 DLPSGKWILQLLAVACLSIAAKIETEVPMLIDLQVGDPOFVFEAKSVORMELLVNLK 173
Db 128 EVPDGKOWMTOLLAVACVSLAAKMEETAAPQCCLDLQVGDARYVFEAKTVQRMELLVTL 187
Qy 174 KWLRLAITPCSVIRYFLRKMSK--CDQEPSNTLISRSLOVIASTTKGIDFLFRPSEAAA 232
Db 188 NWRHVAHTPFSYDYLFLNKLNGSGSTAPRSCWLLQSAELILRAARGTCVGFSEIAAA 247
Qy 233 VALSVSGELQR-----VHFNSPFLSLIQLKERVKKIGEMIESDGSCLC----- 278
Db 248 VAAAVAGVDVDDAGVENACCAHVD-----KERVLCORBAIGSMASAAIDGDA 295
Qy 279 -----SQTNGVLEVSACCFSKTHDSSSS 303
Db 296 TVPPKSARRRSSPVFPVPQSPVGVLD--AAACLSVRSSEAAATA 339

RESULT 6

US-09-404-296B-28
; Sequence 28, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404.296B
; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-404-296B-28

Query Match 28.0%; Score 443.5; DB 4; Length 335;
Best Local Similarity 37.0%; Pred. No. 1.1e-42;
Matches 117; Conservative 53; Mismatches 105; Indels 41; Gaps 11;

Qy 7 ELSLLCTESNVDDEGMIVDETPIEISIPQMGFSQSSESE----EIMENVEKEKQHLPSDD 62
Db 19 DMDLFCGE---DSGVFSGESTVD-----FSSEVDSWPGDSIACFIEDERHFVPGHD 67
Qy 63 YIKELRGDGLDNLNVRDNLNWKACEVHQFGLCFCLAMNYLDRFLSVHDLPSGKWI 122
Db 68 YLSRFQTRSLDAS--AREDSVAMILKQAYNFQPLTAYLVNDRFLYARRLPETSQWP 126
Qy 123 LQLLAVACLSIAAKIETEVPMLIDLQVGDPOFVFEAKSVORMELLVNLKWLRLAITP 182
Db 127 MQLLAVACLSIAAKMEBILVPSLDFQVAGVKYLFEAATIKRMELLVSLVLDMLRSVTP 186
Qy 183 CSVIRYFLRKMSKCDQEPSNT---LISRSLOVIASTTKGIDFLFRPSEAAAVALSVS 238
Db 187 FDFISFPAYKI-----DPSGTFLGFFISHATEIILSNIKASFLFEPWSSIAAAAILCVA 241
Qy 239 GELQRVHFDNSFSPLFSL-----LQKERVKKIGEMIES---DGSCLCSQTPNGV--LE 287
Db 242 NELPSL---SSVNVPHSPETWCGLSKEXIVRCVRLMKAMAIENRL--NTPKVIKLR 296
Qy 288 VSACCFSKTHDSSSS 303
Db 297 VSVRASSTLRPSDES 312

RESULT 7

US-09-404-296B-8
; Sequence 8, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404.296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-09-404-296B-8

Query Match 27.8%; Score 440.5; DB 4; Length 315;
Best Local Similarity 36.6%; Pred. No. 2.3e-42;
Matches 111; Conservative 59; Mismatches 102; Indels 31; Gaps 9;

Qy 10 LLCTESNVDDEGMIVDETPIEISIPQMGFSQS--ESEEIMEMVEKEKQHLPSDDYIKRLR 68
Db 12 LLCE-----DSGILSGDDRPECS---YDFEYSGDFDSDIAEFIEQERKFVPGIDYVERFQ 64
Qy 69 SGDLNVRDNLNWKACEVHQFGLCFCLAMNYLDRFLSVHDLPSGKWILQLLAV 128
Db 65 SQVLDAS--AREDSVAMILKQVRFYGFQPLTAYLVSNVYLDRLFYCRGFPVANGWPLQLLSV 123
Qy 129 ACLSLAAKIEETEVPMLIDLQVGDPOFVFEAKSVORMELLVNLKWLRLAITPCSVIRY 188
Db 124 ACLSLAAKMEETIPLSILDLQVEGAKYIFEPKTRIRMEFLVSLVLDMLRSVTPFSFIFG 183
Qy 189 FLKMSKCDQEPSNT---LISRSLOVIASTTKGIDFLFRPSEAAAVALSVSGELQV 244

Db 184 FSHKI-----DPSGMYTGLISRAQIILSNIOEASLLEYWPCIAAATILCAASDLSKF 238
QY 245 HFDNSFSPLF-SLQKERVKKIGEMIESDGLCSQTPNGV---LEVSACCFSPKTHDS 300
Db 239 SLINADHABSCWCDGLSKKIKTCYRLV-----QSPKILPVHVRVMTARVSTESGDS 289
QY 301 SSS 303
Db 290 SSS 292
RESULT 8
US-09-404-296B-32
; Sequence 32, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-404-296B-32
Query Match 25.1%; Score 398; DB 4; Length 376;
Best Local Similarity 32.9%; Pred. No. 2.6e-37;
Matches 106; Conservative 58; Mismatches 96; Indels 62; Gaps 11;
QY 9 SLICTESNVDEGMIVDETP--IEISIPQMGFSQS-----ESELIMWVEKEKQHLPSDDY 63
Db 21 ALYCEEKWDDEGEVEENSLSSSSPFVLQDLFWDEDEDLVTLFSKEERQGLSCLD- 79
QY 64 IKRLSGDLDLNVRDLDALNIWKAACEVHGFGLCFCLAMNYLDRFLSVHDLPSGKGWIL 123
Db 80 -----DVLSTDRKEAGWILRVNAHGFSTLAALVATYLDKFCISYQROKPMML 132
QY 124 QLLAVACLAAKIBETEYPMILDLQVGPQVFVEAKSVORMELLVINKLWRLRAITPC 183
Db 133 QLVSVACLAAKVEETQVPLLDLQVETKVFVEAKTIQRMELLILSTLEWKHLITPI 192
QY 184 SVIRFPLRK-----MSKCDQEPNTLISRLQVIATTKGIDFLFRPSEAAA 232
Db 193 SFVDHIIRLGLKNNHWDPIAKCH-----RLLSVSDSRFVGLPSVAAA 240
QY 233 VALSVSGELQRVHFNSSP-SPLFSLIQ--KERVKKIGEMIESDGLCSQTPNGVLEVS 289
Db 241 TWMRIIEQVD--PFDPFLSYQTNLLGVNLTKKVKTC-----YDLILQLP-----VD 285
QY 290 ACCFSF-----KTHDSSSS 303
Db 286 RICLQIQSSKRRKSHDSSSS 307

RESULT 9
US-09-404-296B-4
; Sequence 4, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT

; ORGANISM: Nicotiana tabacum
US-09-404-296B-4
Query Match 23.9%; Score 379; DB 4; Length 373;
Best Local Similarity 31.0%; Pred. No. 4e-35;
Matches 113; Conservative 65; Mismatches 94; Indels 92; Gaps 17;
QY 4 ENLELS-----LLCTESN-----VDEGMIVDETPI--EIS-----IQOM 36
Db 7 EQQELSQSFLDLALYCEEBEKEKQHLPSDDYIKRLSGDLDLNVGRDLDALNIWKAACEVHQ 63
QY 37 GFSQS---ESELIMWVEKEKQHLPSDDYIKRLSGDLDLNVGRDLDALNIWKAACEVHQ 93
Db 64 LLEQDLFWDEDELSLFSKEKETHCFWNSF-----QDSSLCSARVDSVEWILKNGVYG 118
QY 94 FGPLCFCLAMNYLDRFLSVHDLPSGKGWILQLLAVACLAAKIBETEYPMILDLQVGP 153
Db 119 FSALTAVLAINVFORFLTSLHVQKDKPMWIQLAAVTCLSLAAKVEETQVPLLDLQVEDA 178
QY 154 QVFVEAKSVORMELLVINKLWRLRAITPCSVIRYFLRKS-----KCDQEPN 202
Db 179 KYVFEAKTIQRMELLVSLKWRMNPVTPLSFLDHIIRLGLRNNIHWFLRRCB---N 234
QY 203 TLISRLQVIATTKGIDFLFRPSEAAAVALSVSGELQ---RVHFDNSSFSPFLSLIQ 259
Db 235 LLLS-----IMADCR-----FVRYPMSVLATAIMLHVHQVEPCNSVDYQNLGLVL--KIN 284
QY 260 KERVKKIGEMIESDGLCSQ-----TPNGVLEVSACCFSKTH-----DS 300
Db 285 KEKVNCFELI---SEVCSKPISHKRYENPSHSPSGWIDP---IYSSSSNDSWDLES 337
QY 301 SSSY 304
Db 338 TSSY 341
RESULT 10
US-09-404-296B-6
; Sequence 6, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-404-296B-6
Query Match 23.4%; Score 370.5; DB 4; Length 367;
Best Local Similarity 32.3%; Pred. No. 3.8e-34;
Matches 97; Conservative 62; Mismatches 84; Indels 57; Gaps 10;
QY 42 ESELIMWVEKEKQHLPSDDYIKRLSGDLDLNVGRDLDALNIWKAACEVHGFGLCFCL 101
Db 58 EDDQLVTLTKKESHLGFDCLIS---DGDGFLVEVRKEALDWMLRVIAHYGFTAMTAVL 114
QY 102 AMNYLDRFLSVHDLPSGKGWILQLLAVACLAAKIBETEYPMILDLQVGPQVFVEAKS 161
Db 115 AVNYDFRVSGLCFQKQKPMWSQLAAVACLAAKIBETEYPMILDLQVADSRVFEAKT 174
QY 162 VORMELLVINKLWRLRAITPCSVIRYFLRK-----MSKCDQEPNTLISRLQ 210
Db 175 IQRMELLVSLTKWKNMNPVTPLSFDHIMRRFGFTNLLHDLFRRCB-----LI---LG 226
QY 211 VIATTKGIDFLFRPSEAAAVALSVSGELQ---RVHFDNSSFSPFLSLQKERVKK-- 265
Db 227 IITDSR-----LLHYPPSVIATAVVYVINEIPECNAMEYQNLMTVL-----KVQDS 275

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; SEQ ID NO 22  
; LENGTH: 349  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-398-858-22
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Query Match 18.4%; Score 291.5; DB 4; Length 349;
Best Local Similarity 31.1%; Pred No. 5.1e-25;
Matches 75; Conservative 43; Mismatches 96; Indels 27; Gaps 5;

QY 10 LLCTESNVD-----DEGMIVDETPIEISIPQMGSQSSEIEIIMMVEKEKH-----L 58
Db 18 LICLEGSDLLADADGA---GTLVWARDERLLVVDQEERYVALLLSKESASGGGPVE 74
QY 59 PSDDIYIKRLSGDLNLNVGRDALNWKACEVHQFGLPCFLAMNYLDRLFVHDLPSG 118
Db 75 EMEWMKAARS-----CVRWIIKTMTAFRFGKGTAYAVNYLDRLFQAORRVNR 124
QY 119 KGWILQLLAVALCLSLAAKIEETEVPMLIDLQVGPPQFVFPEAKSVORMELLVINKLR 178
Db 125 HAWGLQLLMVACMSLATKLEEHAPRLSELPLDACEFAFDRAVLRMELLVLTLEWRMV 184
QY 179 AITPCSIRYIFURKMSKDQEPSNTLISRLOVTASTTKGIDFLEFRPSEAAAAVALSVS 238
Db 185 AVTPFPYISCFAARFR---QDERRAVLVRAVECVFAAIRAMSSVEYQESTIAVASILVAR 241
QY 239 G 239
Db 242 G 242

RESULT 13
US-08-770-761A-2
Sequence 2, Application US/08770761A
Patent No. 5814503
GENERAL INFORMATION:
APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,761A
FILING DATE: 19-DEC-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-770-761A-2

QY 266 -----IGEMIESDGLCSQ-----TPNGVLEVSACCFKTHDSSSYTHLS 308
Db 276 FEERCHOLILELGMTGYNICQLSKRKHQSPGVSDAYFSCDS--SNDWSVASSIS 333

RESULT 11
US-09-404-296B-10
Sequence 10, Application US/09404296B
Patent No. 6559358
GENERAL INFORMATION:
APPLICANT: MURRAY, James Augustus Henry
TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
FILE REFERENCE: 2124-0151P
CURRENT APPLICATION NUMBER: US/09/404,296B
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patent in version 3.1
SEQ ID NO 10
LENGTH: 357
TYPE: PRT
ORGANISM: Helianthus tuberosus
US-09-404-296B-10

Query Match 22.6%; Score 357.5; DB 4; Length 357;
Best Local Similarity 31.1%; Pred. No. 1.2e-32;
Matches 101; Conservative 65; Mismatches 114; Indels 45; Gaps 12;

QY 9 SLICTES-----NVUDE---GMIVDETPIEISIPQMGSQSSEIEIIMMVEKEKQ 56
Db 14 TLFNCNQDHVHEYEYEDFTQTTLTSDSLHLPLDQLDLSWEHELVSFLTKEBQQ 73
QY 57 -HLPSSDIYIKRLSGDLNLNV--GRRDALNWKACEVHQFGLPCFLAMNYLDRLFVSH 113
Db 74 KQTPC-----TLSPFKTSVPAARKEADVWLKVCYGFPTPLTALAINYLDRFLSSL 128
QY 114 DLPSGKGWILQLLAVALCLSLAAKIBETEPMLIDLQVGPPQFVFPEAKSVORMELLVNKL 173
Db 129 HFQEDKPMMIQLVAVSCLSAAKVETQVPLLILDQVEDTKYLFEAKNIQKVELVMSTL 188
QY 174 KWLRAITPCSIRYIFURKMSKDQEPSNTLISRLOVTASTTKGIDFLEFRPSEAAA 233
Db 189 KWRNPVTFISFLDVHVRRLGLTDHVWD-FPKCEAMLCLVDSRSFVCKXPVLATAT 247
QY 234 ALSVGBELQRVHDNSFSPLFLSQ-KERVKKIGEMI-----ESDGDLCQ 280
Db 248 MLHWDEIDPPNCIDYK-SQLDLLTKTDKODINECYVELLAYDHNKRKHDAETTNN 306
QY 281 --TPNGVLEVSACCFKTHDSSS 303
Db 307 PVSPAGVIDF-----TCDESN 323

RESULT 12
US-09-398-858-22
Sequence 22, Application US/09398858
Patent No. 6518487
GENERAL INFORMATION:
APPLICANT: Lowe, Keith S.
APPLICANT: Tao, Yumin
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gregory, Carolyn A.
APPLICANT: McElver, John A.
APPLICANT: Hoerster, George J.
TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
FILE REFERENCE: 0926
CURRENT APPLICATION NUMBER: US/09/398,858
CURRENT FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 60/101,551
PRIOR FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0


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; STRANDEDNESS: single
; TOPOLOGY: linear
; . MOLECULE TYPE: peptide
US-08-464-517-20

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Best Local Similarity 28.4%; Pred. No. 8.1e-19;
Matches 93; Conservative 52; Mismatches 115; Indels 42; Gaps 13;

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Db 1 MENQLLCCVEY-----ET-IRRAYPDNTLL---NDRVLRAMLTEETCAPSVSYFK 46
QY 66 RLRSGLDLNVGRDRLNWIWKACEVHQFGPLCFCLAMNYLDRFLSPSGKGMILQL 125
Db 47 CVQKEIVPSM--RKIVATNMWLEVCESQKCEEVFPPLAMNYLDRFLSLEPLKSR---LQL 101
QY 126 LAVACLSLAAKIETEVPMLDIOVGDPQVFFAKSVQ-----RMELLVLNKLKWRIRAI 180
Db 102 LGATCMFVASKMKEI-IPL-----TABKLCIYTDNSIRPELLQMEULLVNKLKWNLAAM 155
QY 181 TPCSYIRYFLRKMSKCDQEPSNTLISRSLQV-TASTTKGIDFLFEFSEAAAAVALSVSG 239
Db 156 TPDDFIEHLSKMP--DAENKQIIRKHAQTIVALCATDVKFTSNPSMVAAG---SMVA 210
QY 240 ELQRVHFDNSFSFLSQKERYKKIGEMIESDGSDL--CSQPNPVGLEVVS 289
Db 211 AMOGLNLG----SPNNFLSYRTHFLPSRVKICDDPCDLRACQEQIEALLRSS 258

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Tue Mar 23 17:02:04 2004

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-246-361A-20

Query Match 15.0%; Score 237; DB 2; Length 295;
Best Local Similarity 28.4%; Pred. No. 8.1e-19;
Matches 83; Conservative 52; Mismatches 115; Indels 42; Gaps 13;
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Db 1 MENQLLCEV-----ET-IRRAYPTNLI---NDRVIRAMLKIEETCAPSVSYFK 46
Qy 66 RLRSGLDLNVRDRDALNWIWKACEVHQFGPLCFCLAMNYLDRLFSLVHDLPSGKGWILQL 125
Db 47 CVQKEIVPSM--RKIVATWMLEVCEEQCEEEVFLAMNYLDRLFSLLEPLKSR---LQL 101
Qy 126 LAVACLSLAKIETEVEPMLIDLQVDPQFVFEAKSVQ-----RMELLVLNKLKRLRAI 180
Db 102 LGATCMFVASMKET-IPL-----TAEKLCIYTDNISIRPEELLOMELLVNLKKNLAAM 155
Qy 181 TPCSVIRYFLRKMSKCDQEPSNTLISRSLOV-IASITKIDFLERPESEAAAAVALSVSG 239
Db 156 TPHEFIEHFLSKMP--DAENKQIRKHAQTFVLCATDVKFINPFSMWVAG---SMVA 210
Qy 240 ELQRVHFDNSSFPLFLSLQKERVKKIGEMIESDGSDL--CSQTPNGVLEVS 289
Db 211 AMQGLNLG----SPNNFLSRVYRTHFLSRVIKCDPDCCLACQEQIEALLESS 258

Search completed: March 23, 2004, 16:40:15
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 16:39:06 ; Search time 50 Seconds

(without alignments)
1595.165 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAENLELSLCTESNVDDDE.....SACCFKTHDSSSYTHLS 308

Scoring table: BLOSUM62

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Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	627.5	39.6	358	15	US-10-409-701-5
3	621.5	39.3	358	14	US-10-320-230-2
4	620.5	39.2	358	14	US-10-320-230-12
5	613.5	38.8	323	12	US-10-425-114-38749
6	595	37.6	345	12	US-10-425-114-53407
7	595	37.6	345	12	US-10-425-114-56939
8	585.5	37.0	340	15	US-10-425-114-49308
9	563.5	35.6	344	15	US-10-310-154-411
10	554.5	35.0	390	14	US-10-320-230-14
11	521.5	32.9	356	15	US-10-310-154-430
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ALIGNMENTS

RESULT 1

US-10-388-269-2

; Sequence 2, Application US/10388269

; Publication No. US2003022121A1

; GENERAL INFORMATION:

; APPLICANT: MURRAY, James Augustus Henry

; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH

; FILE REFERENCE: 2121-0151P

; CURRENT APPLICATION NUMBER: US/10/388,269

; CURRENT FILING DATE: 2003-03-12

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 2

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Nicotiana tabacum

US-10-388-269-2

Query Match 45.6%; Score 722.5; DB 15; Length 354;

Best Local Similarity 48.1%; Pred. No. 2.5e-67;

Matches 164; Conservative 60; Mismatches 76; Indels 41; Gaps 10;

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Db	61	LSECLSPFWQREMEFLPKDDYVERLRSGDLDLSV-RKEALDWLKAHHYGFGLSFL	119
Qy	102	AMNYLDRFLSVHDLPSKGWILQLLAVACLSLAKEETEVPMLIDLVQGDPOFVFEAK	161
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Db	180	IQRMELLVTLTKWRMAYPTFTFYDFYMKNGG-DOIPSRPLISGMSQLILSIISIDF	238

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; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701163268_FLI.pep
US-10-425-114-56939

Query Match      37.6%; Score 595; DB 12; Length 345;
Best Local Similarity 44.3%; Pred. No. 7e-54;
Matches 132; Conservative 49; Mismatches 87; Indels 30; Gaps 7;

QY 1 MAENLELS---LLCTE---SNVDDGMIIVDETPF-----EISIPQMGSQSESE 44
Db MAPSSYEVAASILLCAEDSSILLDEAEAEAEALLARSGEPPGGABFPVP-----SE 105
QY 45 EIIMENVEKEKQHLPSDDYIKRLSGDLINVCRRDALNWKACVHGFPLCFCLANN 104
Db 106 ECVAGFLESEAAHMPREDYAEALRSRSGMDLRV-RTDAIDWIKVHYCYGFGPLTACLVN 164
QY 105 YLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIEETEVPMLDLQVGDPOFPEAKSVOR 164
Db 165 YLDRFLSVLQPLPGKAWMTQLLSVACLSLAAKMEETYVPSSLDLQAGDARYVFEKTIOR 224
QY 165 MELLVUNKLWRRAITPCSYIRYFURKMSKCDQEPSNTLISRLQVIASTTKGIDFLBF 224
Db 225 MELLVSLTKRMOAVTPLSYVDYFLHRL-RGGAAPSRRAVLSAEILLIARGTCLDF 283
QY 225 RSEERAAVAALSVSGELQRVHFDNSFSPLFSLLOKERVKKIGEMIESDGLCSQTP 282
Db 284 RFEISALAAVAATVAGERAVDIDRA----FTHRVHKEVRSRCLEAIQATATMALPOP 337

RESULT 8
US-10-425-114-49308
; Sequence 49308, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49308
; TYPE: PRT
; FEATURE:
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: 700102335_FLI.pep
US-10-425-114-49308

Query Match      37.0%; Score 585.5; DB 12; Length 340;
Best Local Similarity 43.7%; Pred. No. 6.9e-53;
Matches 135; Conservative 45; Mismatches 86; Indels 43; Gaps 8;

QY 1 MAENLEL---SLCTESNVDDGMIVD-----ETPIBISIPQM 37
Db 50 MAPSSYEMAATLLCGE---DSSSILLDEAGQEEBEEVLLARSRTGRGSEVVPVP--- 102
QY 38 FSQSESEIIMWVEKEKQHLPSDDYIKRLSGDLINVCRRDALNWKACVHGFPL 97
Db 103 -----SEDCVAGFVEAEAAHMPREDYAEALRSRSGMDLRV-RTDAIDWIKVHYCYGFGPL 156
QY 98 CFCLANVLDRLFSVHDLPSGKGWILQLLAVACLSLAAKIEETEVPMLDLQVGDPOFVF 157
Db 157 TACLANNVLDRLFSVHDLPSGKGWILQLLAVACLSLAAKIEETEVPMLDLQVGDPOFVF 216
QY 158 EAKSVORMELLVNLKWLRLRAITPCSYIRYFURKMSKCDQEPSNTLISRLQVIASTTK 217

; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701163268_FLI.pep
US-10-425-114-56939

Query Match      37.6%; Score 595; DB 12; Length 345;
Best Local Similarity 44.3%; Pred. No. 7e-54;
Matches 132; Conservative 49; Mismatches 87; Indels 30; Gaps 7;

QY 1 MAENLELS---LLCTE---SNVDDGMIIVDETPF-----EISIPQMGSQSESE 44
Db MAPSSYEVAASILLCAEDSSILLDEAEAEAEALLARSGEPPGGABFPVP-----SE 105
QY 45 EIIMENVEKEKQHLPSDDYIKRLSGDLINVCRRDALNWKACVHGFPLCFCLANN 104
Db 106 ECVAGFLESEAAHMPREDYAEALRSRSGMDLRV-RTDAIDWIKVHYCYGFGPLTACLVN 164
QY 105 YLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIEETEVPMLDLQVGDPOFPEAKSVOR 164
Db 165 YLDRFLSVLQPLPGKAWMTQLLSVACLSLAAKMEETYVPSSLDLQAGDARYVFEKTIOR 224
QY 165 MELLVUNKLWRRAITPCSYIRYFURKMSKCDQEPSNTLISRLQVIASTTKGIDFLBF 224
Db 225 MELLVSLTKRMOAVTPLSYVDYFLHRL-RGGAAPSRRAVLSAEILLIARGTCLDF 283
QY 225 RSEERAAVAALSVSGELQRVHFDNSFSPLFSLLOKERVKKIGEMIESDGLCSQTP 282
Db 284 RFEISALAAVAATVAGERAVDIDRA----FTHRVHKEVRSRCLEAIQATATMALPOP 337

RESULT 9
US-10-310-154-411
; Sequence 411, Application US/10310154
; Publication No. US20030233670A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Aneeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhuo
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanquo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 411
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Zea mays
```



```
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-310-154-430

Query Match      32.9%; Score 521.5; DB 15; Length 356;
Best Local Similarity 44.4%; Pred. No. 4.2e-46;
Matches 119; Conservative 49; Mismatches 89; Indels 11; Gaps 6;

QY 42 ESEIIMEVVEKEKQHLPSDDYIKRLSGDLNNGRRDALNWIWKAQVHGFPLCFCL 101
DB 60 DSEDFVALLVEKMDHQPGYGLKLELGLGLECS-WRKDAIDWICKHYHNGPGLSULY 118
QY 102 ANMYLDRFLSVHDLPSGKGWILQLLAVACLISLAAKIEETEVEPMLIDLQVGDPOVFPEAKS 161
DB 119 AVNYLDRFLSSFNPLPHDESWMQQLSVCSLSLATKMEETVWPLPMDLQVDFDAEYVEARH 178
QY 162 VQRMELLVNLKWLRLRAITPCSYIRYFLRKMCKDOEPSNTILSRSLQVIASTTKGIDF 221
DB 179 IKEMELIVMKTLLKRLQAVTPFSFYGFLDKFNE-GKPPSYTLASWCSDLTGVTGLKDSRF 237
QY 222 LEPRPSEAAAVALSVSGELORVHFONSPSPFLSLLOKERVKKIGE-MIES-----DG 274
DB 238 LSPRPSEIAAAVVLAVLAENQFLVF-NSALGESEIPVNMKMWRCYELMWVKALVKIRN 296
QY 275 SDCSQTPNGVLEV-SACCFSEFKTHDS 301
DB 297 SNASSVPHSPITVLDAAACFSPSRDDTT 324

RESULT 12
US-10-424-599-273602
; Sequence 273602, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 273602
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)..(251)
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89084C.1.pep
US-10-424-599-273602

Query Match      31.6%; Score 501; DB 12; Length 251;
Best Local Similarity 44.7%; Pred. No. 3.7e-44;
Matches 119; Conservative 43; Mismatches 58; Indels 46; Gaps 7;

QY 55 KQHLPSDDYIKRLSGDLNNGRRDALNWIWKAQVHGFPLCFCLAMNYLDRFLSVHD 114
DB 7 EENLPQDGYLKRLLSGDLDSV-RKEALDWIK----- 38
QY 115 LPSGKGWILQLLAVACLISLAAKIEETEVEPMLIDLQVGDPOVFPEAKSVQRMELLVNLKJ 174
DB 39 --RGSWSMQLLAVACUSIAAMEIKVPPCVDQLXPKFAFPAKDIQRMELLVSTLR 96
QY 175 WRLRAITPCSYIRYFLRKMCKDOEPSNTILSRSLQVIASTTKGIDFLEFRPSEAAA 234
DB 97 WKMQASFPFSLDYFLAKIT-CDQVIVKSSILRSVGPLNLIKCNFLFRPSEIAA 155

; LENGTH: 356
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-310-154-430

Query Match      32.9%; Score 521.5; DB 15; Length 356;
Best Local Similarity 44.4%; Pred. No. 4.2e-46;
Matches 119; Conservative 49; Mismatches 89; Indels 11; Gaps 6;

QY 42 ESEIIMEVVEKEKQHLPSDDYIKRLSGDLNNGRRDALNWIWKAQVHGFPLCFCL 101
DB 60 DSEDFVALLVEKMDHQPGYGLKLELGLGLECS-WRKDAIDWICKHYHNGPGLSULY 118
QY 102 ANMYLDRFLSVHDLPSGKGWILQLLAVACLISLAAKIEETEVEPMLIDLQVGDPOVFPEAKS 161
DB 119 AVNYLDRFLSSFNPLPHDESWMQQLSVCSLSLATKMEETVWPLPMDLQVDFDAEYVEARH 178
QY 162 VQRMELLVNLKWLRLRAITPCSYIRYFLRKMCKDOEPSNTILSRSLQVIASTTKGIDF 221
DB 179 IKEMELIVMKTLLKRLQAVTPFSFYGFLDKFNE-GKPPSYTLASWCSDLTGVTGLKDSRF 237
QY 222 LEPRPSEAAAVALSVSGELORVHFONSPSPFLSLLOKERVKKIGE-MIES-----DG 274
DB 238 LSPRPSEIAAAVVLAVLAENQFLVF-NSALGESEIPVNMKMWRCYELMWVKALVKIRN 296
QY 275 SDCSQTPNGVLEV-SACCFSEFKTHDS 301
DB 297 SNASSVPHSPITVLDAAACFSPSRDDTT 324

RESULT 13
US-10-424-599-226651
; Sequence 226651, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 226651
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)..(229)
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_46697C.1.pep
US-10-424-599-226651

Query Match      30.7%; Score 486; DB 12; Length 229;
Best Local Similarity 47.2%; Pred. No. 1.2e-42;
Matches 102; Conservative 36; Mismatches 46; Indels 32; Gaps 5;

QY 9 SLLCTESNVDDSGMIVDETPI-----EISIPQMGFGQSESE 44
DB 10 SLLCVEDN-----SIFDENDYGSVEVLEDAWQDPYRRNLSQSENLDVFN-GWFLQSD 63
QY 45 EIMEMVVEKEKQHLPSDDYIKRLSGDLNNGRRDALNWIWKAQVHGFPLCFCLAMN 104
DB 64 ECLRLMVEKEWDHLPNGDYRNKLSRGDLDFE-ARKEAIDMIQKVQEHFGFVPCAYLSIN 122
QY 105 YLDRFLSVHDLPSGKGWILQLLAVACLISLAAKIEETEVEPMLIDLQVGDPOVFPEAKSVOR 164
DB 123 YLDRFLSAIYELPHRTWTWQLLAVGCLSLAAKMEETDAPMSLDLQVGESKYIFEAKTOR 182
QY 165 MELLVNLKWLRLRAITPCSYIRYFLRKMCKDQEP 200
DB 183 MELLVNLSTLRMRMQAITPXSFIDHFLYKIND-DQSP 217

RESULT 14
US-10-424-599-218205
; Sequence 218205, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 218205
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Job time : 58 secs

```
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_39067C.1.pep
US-10-424-599-218205

Query Match      30.3%; Score 480; DB 12; Length 309;
Best Local Similarity 41.5%; Pred. No. 8.2e-42;
Matches 110; Conservative 44; Mismatches 83; Indels 28; Gaps 7;

QY 44 EEIIMVVEKEKQHLPSDDYIKRLSGDLDLVNVRDALNWIWKADEVHGFGLCFCLAM 103
DB 20 EAATAGLLDAPHPMPKDYLRRCRDSVDV-TARLDVAVWILKVHAYYEFSPVTAFLSV 78

QY 104 NYLDRFLSVHDLF--SGKGWILQLLAVACLAAKIEETEVPMLIDLVQGDPOQVFEAKS 161
DB 79 NYDFRFLSRCGLPQSG-GWAFQLSVACLAAKMEESHVPFLDLQLFEPKVFPEPKT 137

QY 162 VORMELLVNLKWLRLRAITPCSVIRYFLRKM-SKCDQEPSNTLISRSLQVIASTTKGID 220
DB 138 IQRMELWYMSNLKWLRLSVTFDFYLRHYFISKLPSSSSQSLNHFSTSSNLILSTTRVIN 197

QY 221 FLEFRPSE-AAAAVAALSVSGELQVRVHFDNSSFSLFSLQKERVYKIGEMIESDGLC- 278
DB 198 FLGAPSTVAAAVLCSANGQLPLSFHD-----IRDEMYRCCQMLMEYVVDTCP 248

QY 279 -----SOTPNGVLEVSAC 291
DB 249 ASIKVRITEAAAPSSPVGLDAATC 273

RESULT 15
US-10-424-599-273603
; Sequence 273603, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 273603
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_89085C.1.pep
US-10-424-599-273603

Query Match      30.2%; Score 477.5; DB 12; Length 238;
Best Local Similarity 58.6%; Pred. No. 1e-41;
Matches 92; Conservative 30; Mismatches 28; Indels 7; Gaps 3;

QY 42 ESEIIMVVEKEKQHLPSDDYIKRLSGDLDLVNVRDALNWIWKADEVHGFGLCFCL 101
DB 89 QSDETVMGLVGRSEHLPHVGYLKRLLSGDLDSV-RKEALDWIKAHAYDFGPGCSLCL 147

QY 102 AMNYLDRFLSVHDLFSGKGWILQLLAVACLAAKIEETEVPMLIDLVQGDPOQVFEAKS 161
DB 148 SVNLYLDRFLSVYELPRGKSNWQLLAVACLAAKMEESHVPFLDLQLFEPKVFPEPKT 202

QY 162 VORMELLVNLKWLRLRAITPCSVIRYFLRKM-SKCDQ 198
DB 203 IQRMELVLSLRKWKQASTTFDFYLRKIT-CDQ 238
```

Search completed: March 23, 2004, 16:45:20

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:35:16 ; Search time 26 Seconds
(without alignments)
1139.500 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAENLELSLLCTESNVNDE.....SACCFSPKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	954	60.3	317	T49995	cyclin protein-lik
2	650.5	41.7	372	T09961	cyclin D-like prot
3	635.5	40.1	361	C84613	probable cyclin D
4	633	40.0	383	S51651	cyclin delta-2 - A
5	443.5	28.0	339	A96725	hypothetical prote
6	434	27.4	334	S51650	cyclin delta-1 - A
7	392	24.8	376	T05420	cyclin delta-3 - A
8	354.5	22.4	386	T09598	cyclin 4, D-type -
9	353	22.3	361	T45860	cyclin D3-like pro
10	305	19.3	302	B5041	probable D-type cy
11	285.5	16.8	321	T04720	hypothetical prote
12	260.5	16.5	291	S57922	cyclin D1 - Africa
13	253	16.0	291	S62730	cyclin D1 - zebra
14	242	15.3	288	T58372	cyclin D2 - rat
15	241	15.2	289	A41984	cyclin D2 - mouse
16	239	15.1	295	A56523	cyclin D1 - mouse
17	236	14.9	295	A38977	cyclin D1 - human
18	235	14.8	295	UJ2342	cyclin D1 - rat
19	232	14.7	289	A42822	cyclin D2 - human
20	231	14.6	288	UJ4011	cyclin D2 - rat
21	224.5	14.2	291	UJ4579	cyclin D2 - chicke
22	220.5	13.9	291	S57925	cyclin D2 - Africa
23	216.5	13.7	502	T02746	cyclin A-like prot
24	204.5	12.9	456	C57742	cyclin II - maize
25	198	12.5	454	A96803	probable mitotic c
26	188.5	11.9	395	A40270	cyclin E - human
27	187.5	11.8	493	T03609	cyclin, A-type - c
28	181.5	11.5	482	T02967	cyclin A-type (clo
29	181	11.4	292	B42822	cyclin D3 - human

30	180.5	11.4	483	2	T02966	cyclin A-type (clo
31	180.5	11.4	483	2	T03606	cyclin, A-type - c
32	175.5	11.1	426	2	S17792	cyclin A - common
33	174.5	11.0	341	2	T48232	hypothetical prote
34	173	10.9	293	2	UJ4012	cyclin D3 - rat
35	171	10.8	428	2	S56679	mitosis-specific c
36	171	10.8	460	2	D96505	probable mitotic c
37	170.5	10.8	372	2	T09962	cyclin A-type - Ma
38	170	10.7	348	2	T07669	cyclin A1-type, mi
39	170	10.7	484	2	T07675	cyclin A2-type, mi
40	168.5	10.6	406	2	S24788	cyclin A - bovine
41	167.5	10.6	314	2	T02964	cyclin A-type (clo
42	167.5	10.6	432	2	S08277	cyclin A - human
43	167	10.5	328	2	S29925	cyclin B6 - yeast
44	167	10.5	380	2	S64417	mitosis-specific c
45	166	10.5	425	2	S53004	mitosis-specific c

ALIGNMENTS

RESULT 1

T49995

cyclin protein-like - Arabidopsis thaliana

N;Alternate names: protein F12B17.210

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C;Accession: T49995

R;Bavan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

A;Reference number: 225026

A;Accession: T49995

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-317 <BEV>

A;Cross-references: EMBL:AL333995; GSPDB:GN00063; ATSP:F12B17.210

A;Experimental source: cultivar Columbia; BAC clone F12B17

C;Genetics:

A;Gene: ATSP:F12B17.210

A;Map position: 5

A;Introns: 78/3; 107/3; 140/3; 221/3; 266/3

Query Match		60.3%	Score 954;	DB 2;	Length 317;
Best Local Similarity		64.8%	Pred. No. 1.7e-74;		
Matches 212;		Conservative 23;	Mismatches 58;	Indels 34;	Gaps 8;
Qy	4	ENLESLLTESNVDD	GMIVDETP	PIEISIPQMGFSQSESE	IIEMVKEKQHLPSDDY 63
Db	3	EFNEPNLV---	SNFDEKSNVDTR---	SIFQMGF-PL	ESEIIVREMIKQHSRPRDY 55
Qy	64	IKRLRSGLDINVGR	DALNWKACEVHQPGL	CFCLANNYLDRFLSVHDL	PSGKGWIL 123
Db	56	LKRLNGDLDFNV-	RIQALGNWKACEELQ	FGPLCICLANNYLDRFLSVHDL	PSGKAWT 114
Qy	124	QLLAVACL	SLAAKIEETEVEPMLID	QVDPQFVFEAKSVORMELLV	NLKLKWLRAITPC 183
Db	115	QLLAVACL	SLAAKIEEINVEPMLQ	VGAFNMFVFEAKSVORMELLV	NLKLKWLRAITPC 174
Qy	184	SYIRYLRKMKCDQ	BPSTNLTISR	LQVIATSTK-----	GIDFLEF 224
Db	175	SYVRYFLSKING	YDQEPHSLVTRSL	QVIATSTTKDRLGLFF	FKGVLIVDVWAGIDFLEF 234
Qy	225	RPEAAAVALS	VSGELQRFVFNDS	SFPLSFLLOKERVKKIGEM	ESDGLCSQTPNG 284
Db	235	RASEIAAAVALS	VSGE----	HFDFKFSFSSSLEKERVKKIGEM	IERDGGSSSSSQTENN 290
Qy	285	-VLEVSACCF-	-SFKTHDSSSYTHLS	308	
Db	291	TVLQPKSR	RRYSHLSLSTASVSS	SLTSLS 317	

RESULT 2

T09961

cyclin D-like protein - red goosefoot
 C:Species: Chenopodium rubrum (red goosefoot)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: T09961
 R:Renz, A.; Fountain, M.; Beck, E.
 submitted to the EMBL Data Library, December 1996
 A:Description: Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotrophic
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-372 <REN>
 A:Cross-references: EMBL:Y10162; NID:e1014005; PID:e290219
 A:Experimental source: 7 day old culture; photoautotrophic cells derived from hypocotyl
 C:Genetics:
 A:Gene: cyclD
 C:Keywords: cell cycle control; cell division control

Query Match 41.7%; Score 660.5; DB 2; Length 372;
 Best Local Similarity 44.1%; Pred. No. 4.1e-49;
 Matches 150; Conservative 63; Mismatches 76; Indels 51; Gaps 10;

QY 10 LLCTESN-----VDDEG-IVDETPIEISIPQM----- 36
 DB 7 LLCAEDNSIPDEVDDNYGVDDVQLQCNLQOCHGNLBNPDDFTLLILLIIKEHFEA 66
 QY 37 ---GFSQSESEIIMEMVEKEKQHLPSDDYIKRLSGDLDLNVRDRDALNWIWKADEVHQ 93
 DB 67 LISGFFVA-NHECLASLFDNERQHLGLDYLKRFNGDLDLG-ARNLVIDWTHKQVSHYN 124
 QY 94 FGPLCFCLAMNYLDRFLSVHDLPSGKGWTLQLLAVACLSLAAKIEETEVPMLIDLOVQDP 153
 DB 125 FGPLCVLVSNDLDRFLSAIEPLP-GKAMWQGLGVLACLSLAAKVDETDVLILLDQVSES 183
 QY 154 QVFEAKSVQRMELLVLNKLKWLRAITPCSYIRYFLRMKSKCDQEPNTLISRLQVIA 213
 DB 184 KVFPEAKTIQRMELLVLNKLKWLRAITPCSYIRYFLRMKSKCDQEPNTLISRLQVIA 213
 QY 214 STTKGIDFLFPPSFAAAVALSVSGELQVHFNDNSSPFLSLQKERVKKIGEMI--- 270
 DB 243 STIKGIDLMFPPSFAAAVALSVTQQTQIVFTDKAFSLTDHVEKERLAKVCBIMHDL 302
 QY 271 ---RSDG---SDLCSTQPNGLVSVACCFSPKTHDSSS 303
 DB 303 RMSRSNGALASTVPQSPIGVLDASA-CLSYKSDTSTT 341

RESULT 3
 C84613
 Probable cyclin D [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: C84613
 R:Liu, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: AB4420; MUID:20083487; PMID:10617197
 A:Accession: C84613
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361 <STO>
 A:Cross-references: GB:AE002093; NID:g4544444; PID:NAD22352.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g2490
 A:Map position: 2

Query Match 40.1%; Score 635.5; DB 2; Length 361;
 Best Local Similarity 42.8%; Pred. No. 5.7e-47;
 Matches 154; Conservative 58; Mismatches 75; Indels 73; Gaps 12;

QY 1 MAENLELSLCTESNVDDGIMVDTPTEI-----SI 33

DB 1 MAE-----NLACGETS-----ESWIINDDDDDINYGCGFTNEIDYHQLFAKDNFGNGSI 52
 QY 34 PQMGFSQSE-SEELIMEMVEKEKQHLPSDDYIKRLSGDLDLNVRDRDALNWIWKADEVHQ 92
 DB 53 PMWGSSSSSLSEDRIKEMLVREIFPCGTDVVKLLSGDLDSV-RNQALDWILKVCACHY 111
 QY 93 QFGPLCFCLAMNYLDRFLSVHDLPSGKGWTLQLLAVACLSLAAKIEETEVPMLIDLOVQDP 152
 DB 112 HFGHLICLSMNYLDRFLSVHDLPSGKGWTLQLLAVACLSLAAKIEETEVPMLIDLOVQDP 171
 QY 153 PQVFEAKSVQRMELLVLNKLKWLRAITPCSYIRYFLRMKSKCDQEPNTLISRLQVIA 212
 DB 172 PKVFEAKTIQRMELLVLNKLKWLRAITPCSYIRYFLRMKSKCDQEPNTLISRLQVIA 228
 QY 213 ASATTKGIDFLFPPSFAAAVALSVSGELQVHFNDNSSPFLSLQKERVKKIGEMI 270
 DB 229 LNTTKAIEFLDFRPSFAAAVALSVSGELQVHFNDNSSPFLSLQKERVKKIGEMI 286
 QY 271 ES-----DQSDLCSTQPNGLVSVACCFSPKTHDSSS 303
 DB 287 RSLTGEENVRGTSLSQEQARVAVRASPVGYLE--ATCLSYRSEERTVESCTNSQSS 344

RESULT 4
 S51651
 cyclin delta-2 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 25-Apr-1997
 C:Accession: S51651
 R:Soni, R.; Camichael, J.P.; Shah, Z.H.; Murray, J.A.H.
 submitted to the EMBL Data Library, December 1994
 A:Description: A family of cyclin D homologs from plants differentially controlled by gr
 A:Reference number: S51650
 A:Accession: S51651
 A:Molecule type: mRNA
 A:Residues: 1-383 <SON>
 A:Cross-references: EMBL:X83370
 C:Keywords: cell cycle control; cell division control

Query Match 40.0%; Score 633; DB 2; Length 383;
 Best Local Similarity 47.7%; Pred. No. 1e-46;
 Matches 144; Conservative 53; Mismatches 67; Indels 38; Gaps 9;

QY 32 SIPQMGFSQSE-SEELIMEMVEKEKQHLPSDDYIKRLSGDLDLNVRDRDALNWIWKADEVHQ 90
 DB 51 SIPMGSSSSSLSEDRIKEMLVREIFPCGTDVVKLLSGDLDSV-RNQALDWILKVCACHY 109
 QY 91 VHQFGPLCFCLAMNYLDRFLSVHDLPSGKGWTLQLLAVACLSLAAKIEETEVPMLIDLOVQ 150
 DB 110 HYHFGHLICLSMNYLDRFLSVHDLPSGKGWTLQLLAVACLSLAAKIEETEVPMLIDLOVQ 169
 QY 151 GDPQVFEAKSVQRMELLVLNKLKWLRAITPCSYIRYFLRMKSKCDQEPNTLISRLQVIA 210
 DB 170 EDPKVPFEAKTIQRMELLVLNKLKWLRAITPCSYIRYFLRMKSKCDQEPNTLISRLQVIA 226
 QY 211 VIATTKGIDFLFPPSFAAAVALSVSGELQVHFNDNSSPFLSLQKERVKKIGEMI 268
 DB 227 FILNTTKAIEFLDFRPSFAAAVALSVSGELQVHFNDNSSPFLSLQKERVKKIGEMI 284
 QY 269 MIES-----DQSDLCSTQPNGLVSVACCFSPKTHDSSS 301
 DB 285 LMRSLTGEENVRGTSLSQEQARVAVRASPVGYLE--ATCLSYRSEERTVESCTNSQSS 342
 QY 302 SS 303
 DB 343 SS 344

RESULT 5
 A96725
 hypothetical protein F20P5.7 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96725
R;Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96725
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <SPO>
A;Cross-references: GB:AE005173; MID:g2194121; PIDN:AA61096.1; GSPDB:GN00141
C;Genetics:
A;Gene: F20P5.7
A;Map position: 1

Query Match	28.0%;	Score	443.5;	DB	2;	Length	339;
Best Local Similarity	37.0%;	Pred. No.	1.8e-30;				
Matches	117;	Conservative	53;	Mismatches	105;	Indels	41;
Gaps	11;						

QY	7	ELSLILCTESNVDDGGMIVDETFPIBISIPQMGFSQSESE---	ETIEMWVEKEKQHLPSDD	62
DB	19	DMDLFCGE---	DSGVFSGESTVD-----FSSSEVDSPGDSIACFIEDERHFVPGHD	67
QY	63	YIKRLRSGDLLNVGRDIALNMIKACEVHQFGPLCFCLAMNYLDRLFSLVHDLPSGKGWI	122	
DB	68	YLSRFQTRSLDAS--AREDSVAMILKVQAYYNFQPLTAYLAVNYMDRFLYARRLPETSGWP	126	
QY	123	LOLLAVACLSLAAKIBETEVPMLDLDQVDDQFVFEAKSVORMELLVNLKWLRLAITP	182	
DB	127	MQLLAVACLSLAAKWEELVPSLDFQVAGVKYLFKATIKRMELLVSLVDWFLRSVTP	186	
QY	183	CSYTRYELRKMSKCDQPSNT---	LTSRSLOVIATSTKGDIDLEFPSPSEAAAVALSVS	238
DB	187	FDFlSFYAYKl---	DPsGfTGLFFfSHAVEfILNLSIKESfASfLEYfWfSSfAAAAfILCVa	241
QY	239	GELQRVHFDNSFSGLFSL-----	LOKERVKKTGEMIES---DGSDLCsOTPGV--LE	287
DB	242	NELPSL---	SSVNPfHSPETWCDGLSKEKIVRCYRLMKANAfENRL--NTPKVIaKLR	296
QY	288	VSACCFsFKTHDSSSS	303	
DB	297	VSVRASSTLlTRPSDES	312	

RESULT 6

S51650
cyclin delta-1 - Arabidopsis thaliana

N:Alternate names: cyclin D homolog

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997

R:Accession: S51650

R:Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
submitted to the EMBL Data Library, December 1994

A:Description: A family of cyclin D homologs from plants differentially controlled by growth

A:Reference number: S51650

A:Accession: S51650

A:Molecule type: mRNA

A:Residues: 1-334 <SON>

A:Cross-references: EMBL:X83369; NID:g603504; PID:g603505

C:Keywords: cell cycle control; cell division control

Query Match 27.4%; Score 434; DB 2; Length 334;
Best Local Similarity 37.2%; Pred. No. 1.2e-29;
Matches 116; Conservative 52; Mismatches 110; Indels 34; Gaps 10;

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QY 7 ELSLLCTESNVDDGGMIVDETPIELISIPQWFGSQSESE-----ELIMEMVEKEKQHLPSDD 62
Db 19 DMDLFCGE-----DSGVFSGESTVD-----FSGSEVDSWPGDSIACFIDEKTFVFGHD 67
QY 63 YIKRLSGDLNLVNGRRDALNWIWKACEVHQFGPLFCFLAMNYLDRLFLSVHDLPSGKGWI 122
Db 68 YLSRFQTRSILDAS-AREDSVAMILKVQAYYNFQPLSAYLAVNVMDFLYARRLLPETSQWP 126
QY 123 LQLLAVACLSLAAKIETEVPMLIDIQVGDPOQVFEAKSVORMELLVLNKLKWLRAITP 182
Db 127 MQLLAVACLSLAAKMBEILVPSLDFQVAGVKYLFKATIKRMELLVLSVLDWRLRSVTP 186
QY 183 CSYIRFLRKMSCDOBPNSNTLISRSIQVIATSTTKGIDFLFEPSPSEAAAAVALSVSGELQ 242
Db 187 FDFISFPAYKIDL--RVFPGSGISPMLOSILSNIKEASFLEYWPSSTAAARAILCVANELP 244
QY 243 RVHFDNSFSPFLSL-----LQERVVKIKGEMIES---DGSDLCSOTPNGV--LEVSAC 291
Db 245 SL---SSVNVPHSPETWC DGLSKEKIVRCYRLMKAMAIENNRL--NTPKVIAKLRVSR 299
QY 292 CFSFKYHDSSSS 303
Db 300 ASSTLRPSDES 311

RESULT 7
T05420
cyclin delta-3 - Arabidopsis thaliana
N;Alternate names: cyclin D homolog; protein F28A23.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05420; S51652
R;Bevan, M.; Weichselgartner, M.; Fartmann, B.; Grandearth, K.; Dauner, D.; Herzl, A.;
submitted to the Protein Sequence Database, October 1998
A;Reference number: Z15415
A;Accession: T05420
A;Molecule type: DNA
A;Residues: 1-376 <BEV>
A;Cross-references: EMBL:AL021961
A;Experimental source: cultivar Columbia; BAC clone F28A23
R;Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
submitted to the EMBL Data Library, December 1994
A;Description: A family of cyclin D homologs from plants differentially controlled by 9
A;Reference number: S51650
A;Accession: S51652
A;Molecule type: mRNA
A;Residues: 1-287,'C',289-370,'R',372-376 <SON>
A;Cross-references: EMBL:X83371; NID:g603508; PID:g603509
C;Genetics.
A;Map position: 4
A;Introns: 158/3; 226/1; 269/3
A;Note: F28A23..80
C;Keywords: cell cycle control; cell division control

Query Match 24.8%; Score 192; DB 2; Length 376;
Best Local Similarity 31.9%; Pred. No. 5.6e-26;
Matches 104; Conservative 60; Mismatches 52; Indels 70; Gaps 10;

QY 9 SLLCTESNVDDGGMIVDETPIELISIPQWFGSQSSE-----ESEIIMEMVEKEKQHLPSDDY 63
Db 21 ALYCEEKWDDEGEVEENSSSSSPFVVLQDLFWEDDLVTLFSKEEQGLSCLD- 79
QY 64 IKRLSGDLNLVNGRRDALNWIWKACEVHQFGPLFCFLAMNYLDRLFLSVHDLPSGKGWIL 123
Db 80 -----DVLSTDRKGAVGWILEVWNAHYGFSTLAAVLAITYLDKFCISYLRDKPWWL 132
QY 124 LQLLAVACLSLAAKIETEVPMLIDIQVGDPOQVFEAKSVORMELLVLNKLKWLRAITPC 183
Db 133 QLVSACLSLAAKVEETQVPLLDQVFEETKYVEAKTIQRMELLILSTLEKWHLITPI 192
QY 184 SYIRFLRK-----MSKCDQBPNSNTLISRSIQVIATSTTKGIDFLFEPSPSEAAAA 232
Db 193 SFVDHITRLGLKNNAHWDFLKNCH-----RLLSVISDSRFGVGLPSVAAA 240

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:31:10 ; Search time 18 seconds
(without alignments)
890.978 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 1583

Sequence: 1 MAENLESLLLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	635.5	40.1	361	1	CGD2_ARATH
2	443.5	28.0	335	1	CGD1_ARATH
3	398	25.1	376	1	CGD1_ARATH
4	260.5	16.5	291	1	CGD1_XENLA
5	253	16.0	291	1	CGD1_BRARE
6	244.5	15.4	292	1	CGD1_CHICK
7	242	15.3	288	1	CGD2_RAT
8	241	15.2	289	1	CGD2_MOUSE
9	239	15.1	295	1	CGD1_MOUSE
10	236	14.9	295	1	CGD1_HUMAN
11	235	14.8	295	1	CGD1_RAT
12	232	14.7	289	1	CGD2_HUMAN
13	224.5	14.2	291	1	CGD2_CHICK
14	220.5	13.9	291	1	CGD2_XENLA
15	188.5	11.9	410	1	CGE1_HUMAN
16	182	11.5	404	1	CGE2_HUMAN
17	181	11.4	292	1	CGE3_HUMAN
18	176	11.1	404	1	CGE2_MOUSE
19	175.5	11.1	426	1	CG2A_PATVU
20	173	10.9	292	1	CGD3_MOUSE
21	173	10.9	293	1	CGD3_RAT
22	172.5	10.9	421	1	CGA1_MOUSE
23	171	10.8	428	1	CG1B_MEDVA
24	170	10.7	465	1	CGA1_HUMAN
25	169.5	10.7	396	1	CGE1_RAT
26	168.5	10.6	406	1	CGA2_BOVIN
27	167.5	10.6	432	1	CGA2_HUMAN
28	167	10.5	328	1	CG2B_MEDSA
29	167	10.5	380	1	CGS6_YEAST
30	165.5	10.5	408	1	CGE1_XENLA
31	165.5	10.5	408	1	CGE2_XENLA
32	164.5	10.4	422	1	CGA2_MOUSE
33	164	10.4	410	1	CG1E_BRARE

34 163.5 10.3 421 1 CGA2_MEDAU
35 163 10.3 434 1 CG2B_MEDVA
36 163 10.3 491 1 CGE1_MOUSE
37 160.5 10.1 491 1 CG2A_DROME
38 159.5 10.1 399 1 CGB2_CHICK
39 159.5 10.1 420 1 CG2A_CHLVR
40 158.5 10.0 408 1 CGE3_XENLA
41 157.5 9.9 392 1 CGB2_RANJA
42 156.5 9.9 418 1 CGA1_XENLA
43 155.5 9.8 395 1 CGA2_CHICK
44 155.5 9.8 419 1 CG2B_ORYSA
45 153.5 9.7 407 1 CGE1_CHICK

ALIGNMENTS

RESULT 1

CGD2_ARATH
ID CGD2_ARATH STANDARD; PRT; 361 AA.
AC P42752, 15-DEC-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin delta-2.
GN CYCD2 OR AT2G22490 OR F14M13.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif";
RL Plant Cell 7:85-103 (1995).
RN [2]
RP REVISIONS.
RA Murray J.A.H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana";
RL Nature 402:761-768 (1999).
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; X83370; CAA58286.1; --
DR EMBL; AC006592; AAD22352.1; --
DR PIR; C84613; C84613.
DR InterPro; IPR006670; Cyclin.


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DR InterPro; IPR004367; Cyclin Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C_1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
SQ SEQUENCE 361 AA; 40579 MW; 6D6DDC7673108D2F CRC64;

Query Match      40.1%; Score 635.5; DB 1; Length 361;
Best Local Similarity 42.8%; Pred. No. 4.2e-46;
Matches 154; Conservative 58; Mismatches 75; Indels 73; Gaps 12;

QY 1 MAENLESLCTENVDDEGMIVDETPIEI-----SI 33
DB 1 MAE-----NLACGTS---ESWIIDNDDDINYGCGFTNEIDYNHQLFAKDDNFGNGSI 52

QY 34 POMGFSQSB-SEIIMEMVEKEKHLPSDDYIKRLSRGDLINVGRRDALNIWKACEVH 92
DB 34 POMGSSSSLSDEKEMLEVRIEFCPTGYVYKRLSLGDLDSV-RNQALDWILKVCAYH 111

QY 93 QFGPLCFCLAMNYLDRFLSVHDLPSGKGIQLLAVACLSLAAKIETEVPMLDLQVGD 152
DB 112 HFGHLCICLSMNYLDRFLSVHDLPSGKGIQLLAVACLSLAAKIETEVPMLDLQVGD 171

QY 153 POFVFEAKSVQRMELLVNLKWLRLAATPCSYIRYFLKMKSCDQEPSNTLISRLQVI 212
DB 172 PKFVFEAKTIKEMELLVNLKWLRLAATPCSYIRYFLKMKSCDQEPSNTLISRLQVI 228

QY 213 ASTTKGIDFLRPSB-AAAAVAHSVSGELQKRVHFDNSFSFLSLQKQKVKIGEMI 270
DB 229 LNTTKAIEFLDRPSEIAAAVAHSVSGELQKRVHFDNSFSFLSLQKQKVKIGEMI 286

QY 271 ES-----DGSDLCSQ-----TPNGVLEVSACCFK-----THDSGSS 303
DB 287 RSLTGENVRGTSLSQEQARVAVRAVPASFGVLE--ATCLSVRGEERTVESCNTSSQSS 344

RESULT 2
CGDI ARATH
ID CGDI ARATH STANDARD; PRT; 335 AA.
AC P42751; O04525;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cyclin delta-1.
GN CYCD1 OR AT1G70210 OR F20P5.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCB_TaxID=3702;
PI [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
RT by growth regulators and containing the conserved retinoblastoma
RT protein interaction motif."
RL Plant Cell 7:85-103 (1995).
RN [2]
RP REVISIONS.
RA Murray J.A.H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway T.H., Dewar K.,

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RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820 (2000).
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83369; CAA58285.1; -.
DR EMBL; AC002062; AAB61096.1; -.
DR PIR; A96725; A96725.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C_1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
FT CONFLICT 313 313 S -> SFSSS (IN REF. 3).
SQ SEQUENCE 335 AA; 37868 MW; D365767F3D2FC639 CRC64;

Query Match      28.0%; Score 443.5; DB 1; Length 335;
Best Local Similarity 37.0%; Pred. No. 5.6e-30;
Matches 117; Conservative 53; Mismatches 105; Indels 41; Gaps 11;

QY 7 ELSLICTESNVDDGMIVDETPIELISIPQMGSQSESE-----EIMEMVEKEKHLPSDD 62
DB 19 DMDLFCGE-----DSGVFSGESTVD-----FSSEVDSWPGDSIACIEDERHVFPGHD 67

QY 63 YIKRLSRGDLINVGRRDALNIWKACEVHFGPLCFCLAMNYLDRFLSVHDLPSGKGI 122
DB 68 YLSRFQTRSLDAS-AREDSVAWILKVQAVYFNQPLTAVLVNMDRFLYARRLPETSGWP 126

QY 123 LQLLAVACLSLAAKIETEVPMLDLQVGDQFVFEAKSVQRMELLVNLKWLRLAATP 182
DB 127 MQLLAVACLSLAAKMEELVPSLDFQVAGVFKFEAKTIKEMELLVSVLDWRLSVTP 186

QY 183 CSYIRYFLKMKSCDQEPSNT-----LISRLQVIASSTTKGIDFLRPSAAAAVAHSV 238
DB 187 PFIFFAYKI-----DFSGTFLGFIISHATEILISNKEASFLEYWSSIAAAILCVA 241

QY 239 GELQRVHFDNSFSFLSL-----LQKRVKIKGEMIES-----DGSDLCSQTPNGV--LE 287
DB 242 NELPSL--SSVNPHEPSPETWCDCGLSKEKIVRCVRLKMAIENNL--NTPKVIKLR 296

QY 288 VSACCFKTHDSGSS 303
DB 297 VSVRASSTLTRESDES 312

RESULT 3
CGDI ARATH
ID CGDI ARATH STANDARD; PRT; 376 AA.
AC P42753; O49489;
DT 01-NOV-1995 (Rel. 32, Created)

```

DT. 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclin delta-3.
 GN CYCD3 OR AT4G34160 OR F28A23.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
 RX MEDLINE=95210930; PubMed=7696881;
 RA Soud R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
 RT "A family of cyclin D homologs from plants differentially controlled
 RT by growth regulators and containing the conserved retinoblastoma
 RL protein interaction motif.";
 RL Plant Cell 7:85-103(1995).
 RN [2]
 RP REVISION TO 371.
 RA Murray J.A.H.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Ansgore W., Brand P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier L., Mache R., Mueller M.,
 RA Kreis M., Delsing M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzenecker T., Bothe G., Ransperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argitoni A., Vitale D., Liguori R., Piravandi E.,
 RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lechhary A., Aubourg S.,
 RA Chafador F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Pedhja N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonou B., Zidan M., Strong C., Sun H., Lanar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
 RA Chen E., Maria M.A., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RL thaliana.";
 RL Nature 402:769-777(1999).
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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 CC -----
 DR EMBL; X83371; CAA58287.1; -
 DR EMBL; AL021961; CAA17556.1; -
 DR EMBL; AL161584; CAB80133.1; -
 DR PIR; T05420; T05420.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin Cterm.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin C; 1.
 DR SMART; SM00385; CYCLIN; 2.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 KW CONFLICT 288 C -> G (IN REF. 3).
 FT SEQUENCE 376 AA; 42747 MW; F88DSB6BC435FAC2 CRC64;
 SQ

Query Match 25.1%; Score 398; DB 1; Length 376;
 Best Local Similarity 32.9%; Pred. No. 4.4e-26;
 Matches 106; Conservative 58; Mismatches 96; Indels 62; Gaps 11;
 QY 9 SLCTESNVDDGIMVDTP--ISIPQMGFSOS---ESBEIEMWVEKSKHLPSSDDY 63
 DB 21 ALYCEEKWDDEGEVENSSLSSSSSFFVVLQDLFWEDDLVTLFSEHEQGLSCLD-79
 QY 64 IKRLSGDLNLVGRDNLNWKACEVHQFGPLCFCLAMNYLDRFLSVHDLPSGKGWIL 123
 DB 80 -----DVLSTDRKEAVGILRWNAHYGFSTLAAVLAITYLDFKFCISYLQDKPWWL 132
 QY 124 QLLAVACLSIAAKTEETVEPMLDLOVCDPQVFEAKSVQRMELLVNLKWLRAITPC 183
 DB 133 QLVSVACLSIAAKVEETQVPLLDFOVEETKYVFEAKTIQRMELLTSTLEWKHLITPI 192
 QY 184 SYIRFYLRK-----MSKCDQSPNTLSRSQVIASTTKGIDFLFRPSEAAA 232
 DB 193 SFVDHIIRLLKKNNAHWDFLNKCH-----RLLSVDSRFRVGYLPSVVA 240
 QY 233 VALSVGELQKRVHFDNSSF-SPLFSLIQ--KERYKIGEMIESDGLCSQTPNGVLEVS 289
 DB 241 TMRRIIEQVD--PFDPISYQTNLLGVNLNLTKEVKTC-----YDLILQLP-----VD 285
 QY 290 ACCFSP-----KTHDSSSS 303
 DB 286 RICLQIQISKKRKHSHDSSSS 307

RESULT 4
 CGD1_XENLA
 ID CGD1_XENLA STANDARD; PRT; 291 AA.
 AC P50755;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D1.
 GN CCND1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cockerill M.J., Hunt T.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.

RESULT 9

CGD1_MOUSE	
IID	CGD1_MOUSE
AC	STANDARD; PRT; 295 AA.
AC	P25322;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	G1/S-specific cyclin D1.
DE	CCND1 OR CYL-1.
GN	Mus musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	NCBI_TaxID=10090;
OC	[1]_SEQUENCE FROM N.A.
RN	MEDLINE=91235305; PubMed=1827757;
RP	Matsumine H., Roussel M.F., Ashmun R.A., Sherr C.J.;
RP	"Colony-stimulating factor 1 regulates novel cyclins during the G1
RT	phase of the cell cycle.";
RL	Cell 65:701-713(1991).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=95293413; PubMed=7774959;
RP	Smith R., Peters G., Dickson C.;
RA	"Genomic organization of the mouse cyclin D1 gene (Cyl-1).";
RA	Genomics 25:85-92(1995).
RL	[3]
RN	SEQUENCE FROM N.A.
RP	STRAIN=129; TISSUE=Mammary gland;
RP	MEDLINE=22388257; PubMed=12477932;
RP	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Maltby S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schurmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC	(start) transition.
CC	-1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC	a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC	imparts substrate specificity to the complex.
CC	-1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC	-----
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CC	-----
CC	EMBL; M64403; AAA37502.1; -
DR	EMBL; S78355; AAB34495.1; -
DR	EMBL; BC044841; AAB44841.1; -
DR	PIR; A56523; A56523.
DR	MGI; MGI:188313; Ccnd1.
DR	GO; GO:0005829; C:cytosol; IDA.

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GI/S-specific cyclin D2.
 GN CCND2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92347851; PubMed=1386336;
 RA Xiong Y., Menninger J., Beach D., Ward D.C.;
 RT "Molecular cloning and chromosomal mapping of CCND genes encoding
 RT human D-type cyclins.";
 RL Genomics 13:575-584(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=93205384; PubMed=8455931;
 RA Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
 RT "Cyclins D1 and D2 are differentially expressed in human B-lymphoid
 RT cell lines.";
 RL Oncogene 8:1049-1054(1993).
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Miyajima N.;
 RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
 RA Rieder M.J., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Miyamoto K.E., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lottolano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RN SEQUENCE OF 1-240 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92347850; PubMed=1386335;
 RA Inaba T., Matsushima H., Valentini M., Roussel M.F., Sherr C.J.,
 RA Look A.T.;
 RT "Genomic organization, chromosomal localization, and independent
 RT expression of human cyclin D genes.";
 RL Genomics 13:565-574(1992).
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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 CC -----
 CC EMBL; M90813; AA51926.1; -;
 DR EMBL; X68452; CAA48493.1; -;
 DR EMBL; D13639; BAA02802.1; -;
 DR EMBL; AF518005; AAM54041.1; -;
 DR EMBL; BC010958; AAH10958.1; -;
 DR EMBL; M88083; AA51928.1; -;
 DR EMBL; M88080; AA51928.1; JOINED.
 DR EMBL; M88081; AA51928.1; JOINED.
 DR EMBL; M88082; AA51928.1; JOINED.
 DR PIR; A42822; A42822.
 DR Genew; HGNC:1583; CCND2.
 DR GK; P30279; -;
 DR MIM; 123833; -;
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF0134; cyclin; 1.
 DR Pfam; PF02984; cyclin; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 KW CONFLICT 166 167 KL -> NV (IN REF. 6).
 FT CONFLICT 224 224 T -> H (IN REF. 6).
 SQ SEQUENCE 289 AA; 33067 MW; E4ESFEF476D76D90 CRC64;
 Query Match 14.7%; Score 232; DB 1; Length 289;
 Best Local Similarity 28.0%; Pred. No. 3e-12;
 Matches 89; Conservative 50; Mismatches 111; Indels 68; Gaps 16;
 QY 8 LSLCTESN-----VDDEGMIVDETIETISIPQMGFSQSESEIIMEMVEKEKQHLPSDD 62
 DB 1 MELLCEVDPVRAVDRLNRD-----DVLQNLITIEERYLPQCS 42
 QY 63 YIKRLSGDLNNGRRDALNIWKAACEVHQFGLCFCLAMNYLDRLFLSVHDLPSKGMW 122
 DB 43 YFKCVQK-DIQPYM-RRWATMWEVCEBQKCEEEVPLAMNYLDRLFLA--GVPTPKSH- 97
 QY 123 LQLLAVACLSLAAKIEETEVPMLIDQVGPQFVFAKSVQRMELL-----VLNKLKWL 177
 DB 98 LQLLGAVCMFLASKLKETS-PL-----TAEKLCIYTDNSIKPQELLEWELVGLKLNWL 151
 QY 178 RAITPCSYIRYFLRKMSKCDQSPNTLSRLQV-IASITTKGIDFLFRPSE-AAAAVAL 235
 DB 152 AAVTPHDFHILRLKPQ--QREKSLIRKHAQTFFALCATDFKFMYPPIATGSGVA 209
 QY 236 SVSGELQRFHFNSSPSPFLSLQK-----ERVKKIGEMIES-----DGS 275
 DB 210 AICGLQDDEEVSLTCDALTELLAKITNTDVCCLKACQEIHAVLLNSLQYRQDQDGS 269
 QY 276 ---DLCSQ--TPNGVLEV 288
 DB 270 KSEDELQDASTPTDVRDI 287
 RESULT 13
 CG22_CHICK
 ID_CG22_CHICK STANDARD; PRT; 291 AA.
 AC P49706;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GI/S-specific cyclin D2.
 GN CCND2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96144302; PubMed=8566807;
 RA Li H., Grenet J., Kidd V.J.;
 RL "Structure and gene expression of avian cyclin D2.";
 RL Gene 167:341-342(1995).
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC
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 CC -----
 DR EMBL; U28980; AAA96955.1; -;
 DR PIR; JC4579; JC4579.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin Cterm.
 DR InterPro; IPR006671; Cyclin N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 KW CYCLIN
 SQ SEQUENCE 291 AA; 33163 MW; 43A7E646AFA3109 CRC64;

 Query Match 14.2%; Score 224.5; DB 1; Length 291;
 Best Local Similarity 30.1%; Pred. No. 1.3e-11;
 Matches 85; Conservative 46; Mismatches 104; Indels 47; Gaps 16;
 QY 8 LSLICTESNVDEGMIVDTPTTETPISIPQMGFSQSEEEIIMEMVEKEKQHLPSDDYIKRL 67
 Db 1 MELLCE-----VD--PMRRALDPFNLLY--DDRVLHLLTTEERYLPQCSYFKCV 47
 QY 68 RSGDLDLN-VGRDALNWIWKAQVHGFGLCFCLAMNYLDRLFLSVHDLPSGKWLQLL 126
 Db 48 QK---DIQPFMRVATWMLVCEEQCEEEVFPFLAMNYLDRLFLAV--VPTRK-CHLQLL 101
 QY 127 AVACLSLAAKIBETEVEFMILDLQVGPDPQVFVFAKSVQRMELL-----VLNKLKWR 181
 Db 102 GAVCMFLASKLKET-IPL-----TAEKLCIYTDNSIKPQELLEWELVVLGKLKWLAAVT 155
 QY 182 PCSYIRYFLRKMSKCDQEPSNTLI---SRSQVIASTTKGIDFLFRPSE-AAAVALSV 237
 Db 156 PHDFEHLIRKULP-----PKDKLILRKHAQTIFALCATDFNFAMYPSPMIATGSGVAAI 211
 QY 238 SGELQVRHFDNS-SFSPFLSLQK-----ERVKIGEMIES 272
 Db 212 CG-LQLDDGURLSGDSLDFLAKITSTVDVCLKACQEQIES 252
 RESULT 14
 CGD2 XENLA
 ID CGD2 XENLA STANDARD; PRT; 291 AA.
 AC P53782;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D2.
 GN CCND2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97380591; PubMed=9237366;
 RA Taieb F., Jessus C.;
 RL "Xenopus cyclin D2: cloning and expression in oocytes and during
 RL early development.";
 RL Biol. Cell 88:99-111(1996).
 CC -!- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -!- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X89476; CAA61665.1; -;
 DR EMBL; X83503; CAA58493.1; -;
 DR PIR; S57925; S57925.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin Cterm.
 DR InterPro; IPR006671; Cyclin N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 KW CYCLIN
 SQ SEQUENCE 291 AA; 32959 MW; 9A290F04F1531E89 CRC64;

 Query Match 13.9%; Score 220.5; DB 1; Length 291;
 Best Local Similarity 27.6%; Pred. No. 2.8e-11;
 Matches 79; Conservative 49; Mismatches 103; Indels 55; Gaps 13;
 QY 8 LSLICTESNV-----DDEGMIVDTPTTETPISIPQMGFSQSEEEIIMEMVEKEKQHLPSDD 62
 Db 1 MELLCEGDTVRRQDPDPALLLD-----DRVLHLLTTEERYLPQCS 42
 QY 63 YIKRLRSGDLDLN-VGRDALNWIWKAQVHGFGLCFCLAMNYLDRLFLSVHDLPSGKWL 121
 Db 43 YFKCVQK---DIQPFMRVATWMLVCEEQCEEEVFPFLAMNYLDRLFLAV--VPTRK-C 96
 QY 122 ILQLLAVACLSLAAKIBETEVEFMILDLQVGPDPQVFVFAKSVQRMELL-----VLNKLKWR 176
 Db 97 HLQLLGAVCMFLASKLKET-IPL-----TAEKLCIYTDNSIKPQELLEWELVVLGKLKWL 150
 QY 177 LRATPQSYIRYFLRKMSKCDQEPSNTLI---SRSQVIASTTKGIDFLFRPSE-AAAA 232
 Db 151 LAAVTPHDFEHLIRKULP-----PKDKLILRKHAQTIFALCATDFNFAMYPSPMIATGS 206
 QY 233 VALSVSGELQVRHFDNS-SFSPFLSLQK-----ERVKIGEMIES 272
 Db 207 VGAICGLQLDVGTSLSGDSLDFLAKITSTVDVCLKACQEQIES 252
 RESULT 15
 CGE1 HUMAN
 ID CGE1 HUMAN STANDARD; PRT; 410 AA.
 AC P24864; Q14091; Q8NFG1; Q92501;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin E1.

GN CCNE1 OR CCNE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE OF 8-410 FROM N.A.
RP MEDLINE=92005673; PubMed=1833068;
RA Koff A., Cross F., Fisher A., Schumacher J., le Guellec K.,
RA Philippe M., Roberts J.M.;
RT "Human cyclin E, a new cyclin that interacts with two members of the
RT CDC2 gene family,";
RL Cell 66:1217-1228(1991).
RN [2]
RN SEQUENCE OF 8-410 FROM N.A.
RP MEDLINE=92005671; PubMed=1833066;
RA Lew D.J., Dulic V., Reed S.I.;
RT "Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
RT function in yeast,";
RL Cell 66:1197-1206(1991).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM E1L).
RP Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM E1L).
RC TISSUE=Placenta;
RX MEDLINE=22389257; PubMed=12477937;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences,";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN SEQUENCE OF 1-42 FROM N.A.
RP MEDLINE=96226347; PubMed=8649818;
RA Geng Y., Eaton E.N., Picon M., Roberts J.M., Lundberg A.S.,
RA Gifford A., Saret C., Weinberg R.A.;
RT "Regulation of cyclin E transcription by E2Fs and retinoblastoma
RT protein,";
RL Oncogene 12:1173-1180(1996).
RN [6]
RN SEQUENCE OF 281-370 FROM N.A.
RA Li H., Lahti J.M., Valentine M., Saito M., Reed S.I., Look T.,
RA Kidd V.J.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RN ALTERNATIVE SPLICING.
RP MEDLINE=94266993; PubMed=8207080;
RA Sewing A., Reenicke V., Buerger C., Funk M., Mueller R.;
RT "Alternative splicing of human cyclin E,";
RL J. Cell Sci. 107:581-588(1994).
RN [8]
RN PHOSPHORYLATION OF THR-395.
RP MEDLINE=97015119; PubMed=8861947;
RA Won K.A., Reed S.I.;

RT "Activation of cyclin E/CDK2 is coupled to site-specific
RT autophosphorylation and ubiquitin-dependent degradation of cyclin E,";
RL EMBO J. 15:4182-4193(1996).
RN [9]
RN TISSUE SPECIFICITY.
RX MEDLINE=99054678; PubMed=9840943;
RA Zariwala M., Liu J., Xiong Y.;
RT "Cyclin E2, a novel human G1 cyclin and activating partner of CDK2 and
RT CDK3, is induced by viral oncoproteins,";
RL Oncogene 17:2787-2798(1998).
CC -I- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -I- SUBUNIT: Interacts with a member of the CDK2/CDK protein kinases
CC to form a serine/threonine kinase holoenzyme complex. The cyclin
CC subunit imparts substrate specificity to the complex. Interacts
CC with retinoblastoma binding protein 3 and retinoblastoma-like
CC protein 1.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=E1L;
CC IsoId=P24864-1; Sequence=Displayed;
CC Name=E1S;
CC IsoId=P24864-2; Sequence=VSP_001253;
CC Note=Lacks 49 residues within the cyclin box and cannot complex
CC with CDK2;
CC -I- TISSUE SPECIFICITY: Highly expressed in testis and placenta. Low
CC levels in bronchial epithelial cells.
CC -I- PTM: PHOSPHORYLATION BY CDK2 TRIGGERS ITS RELEASE FROM CDK2 AND
CC DEGRADATION VIA THE UBIQUITIN PROTEASOME PATHWAY (BY SIMILARITY).
CC -I- SIMILARITY: Belongs to the cyclin family. Cyclin E subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; M73812; -; NOT ANNOTATED CDS.
DR EMBL; M74093; -; NOT ANNOTATED CDS.
DR EMBL; AF518727; AA554043.1; ALT_INIT.
DR EMBL; BC035498; AA35498.1; -.
DR EMBL; X95406; CAA64687.1; -.
DR EMBL; X95406; CAA64688.1; -.
DR EMBL; U40788; AAA83269.1; -.
DR EMBL; U40787; AAA83269.1; JOINED.
DR PIR; A40270; A40270.
DR Genew; HGNC:1589; CCNE1.
DR GK; P24864; -.
DR MIM; 123837; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0000082; P:G1/S transition of mitotic cell cycle; NAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Alternative splicing;
DR Phosphorylation; Nuclear protein.
FT MOD_RES 395 395 PHOSPHORYLATION.
FT VARSPIC 154 196 Missing (in isoform E1S).
FT CONFLICT 281 281 /FTid=VSP_001253.
FT SEQUENCE 410 AA; 47077 MW; 424DF0B253B7047E CRC64;
FT L -> M (IN REF. 5).
Query Match 11.9%; Score 188.5; DB 1; Length 410;
Best Local Similarity 26.0%; Pred. No. 2.1e-08;
Matches 71; Conservative 49; Mismatches 102; Indels 51; Gaps 12;

Search completed: March 23, 2004, 16:38:03
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:34:50 ; Search time 46 Seconds
(without alignments)
2112.600 Million cell updates/sec

Title: US-09-530-209A-2
Perfect score: 1583
Sequence: 1 WAEENLESLCTESNVDD.....SACFSFKYTHDSSSYTHLS 308

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1583	100.0	308	10 Q9XFR7	Q9xfr7 arabidopsis
2	1579	99.7	308	10 Q9FKP7	Q9fkp7 arabidopsis
3	1565	98.9	308	10 Q8LGA1	Q8lga1 arabidopsis
4	954	60.3	317	10 Q9LX96	Q9lx96 arabidopsis
5	722.5	45.6	354	10 Q9ZRX9	Q9zrx9 nicotiana t
6	660.5	41.7	372	10 P93103	P93103 chenopodium
7	653.5	41.3	382	10 Q8L6U0	Q8l6u0 daucus caro
8	621.5	39.3	358	10 Q8S524	Q8s524 zea mays (m
9	614.5	38.8	356	10 Q8SBC0	Q8sbc0 oryza sativ
10	554.5	35.0	390	10 Q8S522	Q8s522 zea mays (m
11	521.5	32.9	356	10 Q8LH88	Q8lha8 oryza sativ
12	440.5	27.8	315	10 Q8GVE0	Q8gve0 helianthus
13	440	27.8	360	10 Q8GS62	Q8gs62 physcomitre
14	409	25.8	350	10 Q7XAB6	Q7xab6 euphorbia e
15	391	24.7	330	10 Q9SNV2	Q9snv2 antirrhinum
16	390.5	24.7	343	10 Q9SNV1	Q9snv1 antirrhinum

17	379	23.9	364	10 Q9SMD5	Q9smd5 lycopersico
18	379	23.9	373	10 Q9ZRX8	Q9zrx8 nicotiana t
19	378	23.9	352	10 Q8LK74	Q8lk74 lagenaria l
20	373.5	23.6	368	10 Q9SXN7	Q9sxn7 nicotiana t
21	370.5	23.4	367	10 Q9ZRX7	Q9zrx7 nicotiana t
22	370.5	23.4	380	10 Q8LK73	Q8lk73 lagenaria l
23	364.5	23.0	198	10 Q8S521	Q8s521 zea mays (m
24	363	22.9	376	10 Q8GZU3	Q8gzuz3 populus tre
25	362.5	22.9	367	10 Q9FGQ7	Q9fgq7 arabidopsis
26	359.5	22.7	355	10 Q7XAB7	Q7xab7 euphorbia e
27	359.5	22.7	384	10 Q82136	Q82136 pisum sativ
28	357.5	22.6	357	10 Q8GVD9	Q8gvd9 helianthus
29	357.5	22.6	378	10 Q9XG63	Q9xg63 medicago sa
30	354.5	22.4	386	10 Q40338	Q40338 medicago sa
31	353	22.3	361	10 Q9SN11	Q9sn11 arabidopsis
32	352.5	22.3	359	10 Q9S7H9	Q9s7h9 lycopersico
33	351.5	22.2	361	10 Q9SNV0	Q9snv0 antirrhinum
34	346.5	21.9	336	10 Q9SMD4	Q9smd4 lycopersico
35	345.5	21.8	371	10 Q84V88	Q84v88 populus alb
36	344	21.7	289	10 Q8GUV7	Q8guv7 populus alb
37	343.5	21.7	308	10 Q8LFW3	Q8lpw3 helianthus
38	323.5	20.4	222	10 Q9XG64	Q9xg64 medicago sa
39	305	19.3	302	10 Q9ZRX04	Q9zrx04 arabidopsis
40	302	19.1	349	10 Q82678	Q82678 chenopodium
41	291.5	18.4	349	10 Q8S523	Q8s523 zea mays (m
42	285.5	18.0	322	10 Q8H339	Q8h339 oryza sativ
43	285.5	16.8	321	10 Q8SZF6	Q8szf6 arabidopsis
44	260.5	16.5	291	13 Q8AVQ4	Q8avq4 xenopus lae
45	255	16.1	291	13 Q8QFP4	Q8qfp4 brachydanio

ALIGNMENTS

RESULT 1

Q9XFR7 PRELIMINARY; PRT; 308 AA.
AC Q9XFR7;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE D-type cyclin.
GN CYC04.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA de Veylder L., De Almeida Engler J., Burssens S., Manevski A.,
RA Lescure B., Van Montagu M., Engler G., Inze D.;
RT "A new D-type cyclin of Arabidopsis thaliana expressed during lateral
root primordia formation."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ131636; CAB41347.1;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 3487 MW; 591ADA3361DDD63D CRC64;

Query Match 100.0%; Score 1583; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e-139;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

QY	301 SSSYTHLS 308	PRELIMINARY;	PRT;	308 AA.
DB	301 SSSYTHLS 308			
RESULT 2				
Q9FKP7				
ID	Q9FKP7	PRELIMINARY;	PRT;	308 AA.
AC	Q9FKP7;			
DT	01-MAR-2001 (TRENBLrel. 16, Created)			
DDT	01-MAR-2001 (TRENBLrel. 16; Last sequence update)			
DDT	01-JUN-2003 (TRENBLrel. 24, Last annotation update)			
DE	D-type cyclin.			
DE	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
NCBI	TaxID=3702;			
NCBI	TaxID=3702;			
RN	[1]			

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[2]
RN  SEQUENCE FROM N.A.
RP  Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA  Feldmann K.; cDNA from Arabidopsis thaliana.;
RA  Submitted (MAR-2002) to the EMBL/GenBank/DBJG databases.
RC  - I SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
RL  EMBL; AY084386; AAM60963.1; -
DR  GO; GO:0005634; C:nucleus; IEA.
DR  GO; GO:0000910; P:cytokinesis; IEA.
DR  GO; GO:0000074; P:regulation of cell cycle; IEA.
DR  InterPro; IPR006670; Cyclin.
DR  InterPro; IPR004367; Cyclin_Cterm.
DR  InterPro; IPR006671; Cyclin_N.
DR  Pfam; PF00134; cyclin; 1.
DR  Pfam; PF02984; cyclin; 1.
DR  SMART; SM00385; CYCLIN; 1.
DR  PROSITE; PS00292; CYCLINS; 1.
KW  Cell cycle, Cell division, Cyclin.
SQ  SEQUENCE 308 AA; 34788 MW; E8077DA1868DCC42 CRC64;

Query Match          98.9%; Score 1565; DB 10; Length 308;
Best Local Similarity 99.0%; Pred. No. 6.3e-138;

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	Matches	305;	Conservative	1;	Mismatches	2;	Indels	0;	Gaps
Qy	1	MAEENLEISLLCTESNVDD	DEGMIVDETP	PIETISIPQMGFSQSE	EEIIMENVEKEKHLS	60			
Db	1	MAEENLEISLLCTESNVDD	DEGMIVDETP	PIETISIPQMGFSQSE	EEIIMENVEKEKHLS	60			
Qy	61	DDYIKRLSGDLDLNVGR	RDALNIWKACEVHQ	GPLCFCLANNYLDRFL	SVHDLPSGKG	120			
Db	61	DDYIKRLSGDLDLNVGR	RDALNIWKACEVHQ	GPLCFCLANNYLDRFL	SVHDLPSGKG	120			

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QY 121 WILLOLAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAI 180
DB 121 WILLOLAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAI 180
QY 181 TPCSYIRYFLRMKSCDQEPNTLISRSLOVIASTTKGIDLEFRPSEAAAAVALSVSGE 240
DB 181 TPCSYIRYFLRMKSCDQEPNTLISRSLOVIASTTKGIDLEFRPSEAAAAVALSVSGE 240
QY 241 LORVHFONSSPFLSLLOKERVKKIGEMIESDGLCSQTPNGVLEVSACCFKTHDS 300
DB 241 LORVHFONSSPFLSLLOKERVKKIGEMIESDGLCSQTPNGVLEVSACCFKTHDS 300
QY 301 SSSYTHLS 308
DB 301 SSSYTHLS 308

RESULT 4
Q9LX96 PRELIMINARY; PRT; 317 AA.
AC Q9LX96;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin protein-like.
GN F12B17.210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bavan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AL353995; CAB89399.1; -.
DR PIR; T49995; T49995.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 317 AA; 35910 MW; 07616F8480927711 CRC64;

Query Match 60.3%; Score 954; DB 10; Length 317;
Best Local Similarity 64.8%; Pred. No. 9.1e-81;
Matches 212; Conservative 23; Mismatches 58; Indels 34; Gaps 8;

QY 4 ENLESLCTESNVDDGMIVDTPIETISIPQMGFSQSEEEIMEMVEKEKQHLPSDDY 63
DB 3 EFMEPNLV---SNFDEKSNVDTR---SIFQMGF-PLESEIVREIMIEKQHSRPDY 55
QY 64 IKRLRSGDLNVRDALNWKACEVHQFGPLCFLAMNYDLRFLSHVDLPSPGKGWIL 123
DB 56 LKRLRGDLDNFV-RIOALGWIWKAEEQFGPLCFLAMNYDLRFLSHVDLPSPGKATV 114
QY 124 QLILAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAITPC 183
DB 115 QLILAVACLSAAKIEETVPMILDLQVGPQVFEAKSVORMELLVINKLWRLRAITPC 174
QY 184 SYIRYFLRMKSCDQEPNTLISRSLOVIASTTK-----GIDFLF 224
DB 184 SYIRYFLRMKSCDQEPNTLISRSLOVIASTTK-----GIDFLF 224

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DB 175 SYRYFLSKINGYDQEPHSLVTRSLQVIASTTKGDRGLGLFFPKGVLIVDWAGIDFLF 234
QY 225 RPSEAAAAVALSVSGELQRVHFNSSPFLSLLOKERVKKIGEMIESDGLCSQTPNG 284
DB 235 RASEIAAAVALSVSGE---HFDFKFSFSSFSLEKERVKKIGEMIERDGGSSSSSPNN 290
QY 285 -VLEVSACCF--SPKTHDSSSSYTHLS 308
DB 291 TVLQFKRRYSHSLSTASVSSSLTSL 317

RESULT 5
Q9ZRX9 PRELIMINARY; PRT; 354 AA.
AC Q9ZRX9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin D2.1 protein.
GN CYCD2.1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9907070; PubMed=9880377;
RA Sorrell D.A., Combettes B., Chaubet-Gigot N., Gigot C., Murray J.A.H.;
RT "Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels
RT of Transcripts in Tobacco Bright Yellow-2 Cells.";
RL Plant Physiol. 119:343-351 (1999).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ011892; CAA09852.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 354 AA; 39714 MW; 18363A0E786E89BF CRC64;

Query Match 45.6%; Score 722.5; DB 10; Length 354;
Best Local Similarity 48.1%; Pred. No. 4.7e-59;
Matches 164; Conservative 60; Mismatches 76; Indels 41; Gaps 10;

QY 1 MAEENL---ELSLCTESNV---DDEGMIVDETPIETISIPQMGFSQ-----S 41
DB 1 MAADNIYDFAVSNLLCTETKSLCFDDVDSLTSQQNIETKSLDLSFNNGIRSEPLIDLFS 60
QY 42 ESEETIMEMVEKEKQHLPSDDYIKRLRSGDLNVRDALNWKACEVHQFGPLCFL 101
DB 61 LSEECLSFVQREMEFLPKDYVERLSRGLDLSV-RKEALDWILKAHMHYGFGLSFCL 119
QY 102 ANNYLDRLFSLVHDLPSGKGWILQLLAVACLSAAKIEETVPMILDLQVGDPOVFPEAKS 161
DB 120 SINYLDRLFSLVHDLPSRKTWTVQLLAVACLSAAKMEETINVELTVDLQVGDPKFVEGKT 179
QY 162 VORMELLVINKLWRLRAITPCSYIRYFLRMKSCDQEPNTLISRSLOVIASTTKGIDF 221
DB 180 IQRMELLVSLTKWRQAYTPFTIDYPMKNG-DQIPSRPLISGWLILSIIRSIDF 238
QY 222 LFRFSEAAAAVALSVSGELQRVHFNSSPFLSL-LQKERVKKIGEMIE----- 271
DB 239 LFRFSEAAAAVALSVSGEIQAKIDKA--MPCFFIHLDKGRVQCKVELIQDLTATITT 296
QY 272 SPSGLCSQTPNGVLEVSACCFKTHD-----SSSYT 305
DB 272 SPSGLCSQTPNGVLEVSACCFKTHD-----SSSYT 305

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Db 297 AAAASLVPSPIGVLE-AAACLSYKSGDRTVGSCTTSHT 336
RESULT 6
P93103 PRELIMINARY; PRT; 372 AA.
AC P93103;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin-D like protein.
GN CYCD1.
OS Chenopodium rubrum (Red goosefoot) (Pigweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Chenopodium.
OX NCBI_TaxID=3560;
RN [1]
RP SEQUENCE FROM N.A.
RA Renz A., Fountain M., Beck E.;
RT "Nucleotide sequence of a cDNA encoding a D-type cyclin from a
RT photoautotrophic cell suspension culture of Chenopodium rubrum L.";
RL Plant Physiol. 0:0-0(10).
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; Y10162; CAA71244.1; -.
DR PIR; T09961;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
KW SEQUENCE 372 AA; 41768 MW; 6D5D1C91A5DB17CF CRC64;
SQ
Query Match 41.7%; Score 660.5; DB 10; Length 372;
Best Local Similarity 44.1%; Pred. No. 3.2e-53;
Matches 150; Conservative 63; Mismatches 76; Indels 51; Gaps 10;
QY 10 LLCTESN-----VDDEGM-IVDETPIEISIPQM----- 36
Db 7 LLCAEDNSSIFDEVDNNGVDDVLIQCNLQQQHGNGRNFDDFTLLILLIIKEHFEA 66
QY 37 ---GFSSQSEEEIEMVEKEKQHLPSDDYIKRLSGDLINVGRRDALNWIWACEVHQ 93
Db 67 LIISGFFVA-NHECLASLFDNERQHLGLDYLRKFRNGDLGLG-ARNLVIDWIKVQSHYN 124
QY 94 FGPLCFCLANNYLDRFLSVHDLPSGKGWIIQLLAVACLAAKTEETVPMILDLQVGDP 153
Db 125 FGPLCVTLVSNYLDRLFSALHELP-GKAWMQLLGAVACLAAKVDVTDVLLDLQVSES 183
QY 154 QFVPEAKSVQRMELLVLNKLKRLRAITPCSYIRYFLRKMSKCDQPSNTLISRSQVIA 213
Db 184 KFVFEAKTIQRMELLVLSTLKWQSVTPPSFDYFLYKLSG-DKMPKSKSLIFQAIQIL 242
QY 214 STTGIDFLEFRPSEAAAVALSVGLQRFHFNDSFSPFLSLLOKERVKKIGEMIE--- 270
Db 243 STIKGIDLMFEPSPSEAAAVALSVTQQTQVIEFTDKAFSLTDRHVEKERLMKCVIEHDL 302
QY 271 ----ESDG---SDLSQTPNGVLEVSACCFKTHDSSS 303
Db 303 RMSSRSNGALASTVPSPIGVLDASA-CLSYKSDDTSTT 341
RESULT 7
Q85L610 PRELIMINARY; PRT; 382 AA.
ID Q85L610
AC Q85L610;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Cyclin D2.
GN CYCD2.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Campanulids; Apiales; Apiaceae; Apioidae; Scandiceae; Daucinae;
OC Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RA Eun C.H., Ko S.M., Matsubayashi Y., Sakagami Y., Kamada H.;
RT "The effect of the peptidyl growth factor, physosulfolinkine-alpha, on
RT the cell cycle progression in carrot non-embryogenic cells.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ496740; CAD43141.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cell cycle; Cell division; Cyclin.
KW SEQUENCE 382 AA; 43354 MW; 797F88528D809170 CRC64;
SQ
Query Match 41.3%; Score 653.5; DB 10; Length 382;
Best Local Similarity 45.5%; Pred. No. 1.5e-52;
Matches 155; Conservative 60; Mismatches 69; Indels 57; Gaps 12;
QY 9 SILCTESN-----VDDEGMIVDETPIEI-SIPQMGSQSEEEIEMKV 51
Db 17 SILCTETNNLCFFDLKARDQDPRDCENVVNSEALICAVP-----LORDEDFVVF 70
QY 52 EKEKQHLPP-----SDDYIKRLSGDLINVGRRDALNWIWACEVHQFGPLCFCLANNYL 107
Db 71 ESKWNPCEPVIFSTD-----RSGELDLGV-RKEALDVIYKAHAHNFGLSVCLAVNYLD 124
QY 108 RFLSVHDLPSGKGWIIQLLAVACLAAKTEETVPMILDLQVGDPQFVFEAKSVORMEL 167
Db 125 RFLSVLEPSGKGWTVQLLAVACLAAKTEETVPMILDLQVGDPQFVFEAKSVORMEL 184
QY 168 LVLNKLKRLRAITPCSYIRYFLRKMSKCDQPSNTLISRSQVIASTTKGIDFLEFRPS 227
Db 185 LVLSTLKWQSVTPPSFDYFLYKLSG-DKMPKSKSLIFQAIQIL 244
QY 228 EAAAVALSVGLQRFHFNDSFSPFLSLLOKERVKKIGEMIE-----SDGSLDLS 279
Db 245 EISAAVAICVTRQAQTLDI-NKAMSNIIIP-VKDRVFKCIEMIQLTLVTETSNVSGRT 302
QY 280 -----QTPNGVLEVSACCFKTHD-----SSSYTHLS 308
Db 303 RAQVPSPIGVLD--AACLSYKSDERTVGSCTTSHT 341
RESULT 8
Q85S24 PRELIMINARY; PRT; 358 AA.
ID Q85S24
AC Q85S24;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE D-type cyclin.
GN CYCD2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

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Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases
CC -I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AB080248; BAB85522.1; --
DR Gramene; Q8SBC0; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 356 AA; 38937 MW; 502AF4EB9CE8BCEA CRC64;

Query Match 38.8%; Score 614.5; DB 10; Length
Best Local Similarity 45.3%; Pred. No. 6e-49;
Matches 134; Conservative 51; Mismatches 72; Indels

Qy 24 VDPTPIBISIPQMFGFSQSESEIIMEVKEKQHLPSDDYIKRLRS
Db 54 VDVGVDFAVP-----SEECVARLIVETADHMPREDYAEURDURAGC
Qy 80 DALNWIWKACEVHQFGLPCFLAMNYLDRLFLSVHDLFSGKWIILQLLALA
Db 105 DAIDWIWKVHSYYSFAPLTACLAVNYLDRLFLSVQLPDGDKMTQTLLALA
Qy 140 TEVPMILDLQVGPDPQVFPEAKSVORMELLIVNKLKWLRAITPCSYRTIR
Db 165 TDVPSQSLDLQVGBERYVFEAKTIQRMELLVLSTLKWRMQAVTPFSYVYVD
Qy 200 PSNTLISRSLQVTASTTKGIDIEFEPSEAAAAVALSVSGELQRVHFD
Db 224 PGRSALLSELLICTARGTECLGFRPSETAAVAAVWGEHAA-----
Qy 260 KERVKKIGEMIESDG-----SDLCSTQTPNGVLEVSACFCF
Db 274 KERMSHCQEVIOAMELHPKSPSPRVFVSSSPRSPTGVLD--AAGCLL

RESULT 10
Q8S522 PRELIMINARY; PRT; 390 AA.
ID AC Q8S522;
ID CD Q8S522;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DT D-type cyclin.
GN CYCD4.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI TaxID=45777;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Hi-II;
RC Tao Y., Lowe K., Gregory C., Coughlan S.J., Gordon-Kamm W.
RT "Isolation of a family of D-type cyclins from maize that is
RT conserved and unique characteristics."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
-I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AF351191; AAL83928.1; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR006671; Cyclin_Cterm.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.

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DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 390 AA; 42016 MW; 1CE006BE20DABF70 CRC64;

Query Match
  35.08; Score 554.5; DB 10; Length 390;
Best Local Similarity 39.1%; Pred. No. 2.8e-43;
Matches 135; Conservative 52; Mismatches 89; Indels 69; Gaps 9;

QY 10 LLCTESNVD---DEGMIVDETEIETISIPQMGFSQS-----ESEEIIMEMVEK 53
Db 13 LLCAEBHSSLLWDE---EEBLEAVRRGRSPGVDGDFGADLPFPQSEKCVAGLVER 68
QY 54 EKQHLPSDDVYIKRLSGDLNLNVRDALNWKACEVHGFGLCFCLANWYLDRLSVH 113
Db 69 ERDMFGPCYGDRLGGGGLCV-RRADVWIKAYTHFRPLTAYLANVYLDRLSVLS 127
QY 114 DLPSGKGWILQLLAVACLSAAKTEETVPMILDLQVDPQFVFEAKSVORMELLVNLK 173
Db 128 EVDGKDMTQLLAVACVLSAAKMEETAVPQCLDLQVGDARYFEAKTVORMELLVLTLL 187
QY 174 KWLRLAITPCSYIRYFLRKMSK-CDQEPSNTLSRSLOVIASTTKGIDFLEFRPSEAAA 232
Db 188 NWRMHAVTPSYDYVFLNKLNSGSGTAPRSCWLLQSAELLRAARGTCVGRFSEIAAA 247
QY 233 VALSVSGELR-----VHFDNSFSLFLLQKERVKKIGEMIESDGLC----- 278
Db 248 VAAAVAGVDVDDAGVENACCAHVD-----KERVLCQEAIGMASSAAIDGDA 295
QY 279 -----SQTPNGVLEVSACFCFKTHDSSSS 303
Db 296 TVPPKSARRRSPVPVPVPGVGVLD-AAACLSYRSEEAATA 339

RESULT 11
Q8LHA8
ID Q8LHA8 PRELIMINARY; PRT; 356 AA.
AC Q8LHA8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P0594D10.18 protein.
GN P0594D10.18.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0594D10."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AP004380; BAC10182.1; -.
DR Gramene; Q8LHA8; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 356 AA; 39176 MW; 8E8A8B8DA7A39BEE CRC64;

Query Match
  32.9%; Score 521.5; DB 10; Length 356;
Best Local Similarity 44.4%; Pred. No. 3e-40;

Matches 119; Conservative 49; Mismatches 89; Indels 11; Gaps 6;

QY 42 ESEEIIMEMVEKEKQHLPSDDYIKRLSGDLNLNVRDALNWKACEVHGFGLCFCL 101
Db 60 DSDEFVALLVEKEMDHPQFQGVLEKLEGLGLECS-WRKDAIDWICKVHSYVNEGPLSLYL 118
QY 102 ANNYLDRLFLSVHDLPSGKGWILQLLAVACLSAAKTEETVPMILDLQVDPQFVFEAKS 161
Db 119 AVNYLDRLFLSVHDLPSGKGWILQLLAVACLSAAKTEETVPMILDLQVDPQFVFEAKS 178
QY 162 VORMELLVNLKWLRLRAITPCSYIRYFLRKMSKCDQEPSNTLSRSLOVIASTTKGIDF 221
Db 179 IRKMLIVNKTUKRLQAVTPFSFGYFLDKFNE-GKPSYTLASWCSDLTWGTLLKDSRF 237
QY 222 LFRFRSEAAAAVALSVSGELQVHFDNSFSLFLLQKERVKKIGE-MIES-----DG 274
Db 238 LSRFPSEIAAAVLAENQFLVF-NSALGSSEIPVNMKEMVRCVELNVERALKVKKIRN 296
QY 275 SLCSTQTPNGVLEV-SACCFSKTHDSS 301
Db 297 SNASSVPHSPITVLDAAACFSRSDTT 324

RESULT 12
Q8GVE0
ID Q8GVE0 PRELIMINARY; PRT; 315 AA.
AC Q8GVE0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cyclin D1.
GN CYCD1.1.
OS Helianthus tuberosus (Jerusalem artichoke).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Asterioideae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4233;
RN [1]
RC SEQUENCE FROM N.A.
RA Freeman D., Murray J.A.H.;
RT "Isolation, characterization and expression of cyclin and cyclin-
RT dependent kinase genes in Jerusalem Artichoke (Helianthus
RT tuberosus)".
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY063460; AAL47479.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
SQ SEQUENCE 315 AA; 35651 MW; 8F35A49F1097C308 CRC64;

Query Match
  27.8%; Score 440.5; DB 10; Length 315;
Best Local Similarity 36.6%; Pred. No. 9.6e-33;
Matches 111; Conservative 59; Mismatches 102; Indels 31; Gaps 9;

QY 10 LLCTESNVDDEGMIVDETEIETISIPQMGFSQS-ESEEIIMEMVEKEKQHLPSDDYIKRLR 68
Db 12 LLCC-----DSGILSGDDRPECS---YDFEYSGDFDSDIAEFIEQERKFPVGDIVVERPQ 64
QY 69 SGDLNLNVRDALNWKACEVHGFGLCFCLANWYLDRLSVHDLPSGKGWILQLLAV 128
Db 65 SQVLDAAS-AEESVAVILKQVRFYGFQPLTAYLSVNYLDRLFYCRGFPVANGWPLQLLSV 123
QY 129 ACLSLAAKTEETVPMILDLQVDPQFVFEAKSVORMELLVNLKWLRLRAITPCSYIRY 188
Db 124 ACLSLAAKMEETLIPSLDLQVEGAKYIPEKTIIRMEFLVSLDRLRSVTPFSFIGF 183

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QY 189 FLKMSKCDQEPSNT-----LISRSQVIASTTKGIDFLFEPSEAAAVALSVSGELQRV 244
D 184 FSHKI-----DPGMYTGLISRATQIILNIQASLELWPSICAAATILCAASDLKSF 238
QY 245 HFNSFSPLF-SLLQKRYKIGEMIESDGLCSQTPNGV---LEVSACCFKTHDS 300
D 239 SLINADHAESWCGLSKEKTKCYRLV-----QSPKILPVHVVMVARTVSTSGDS 289
QY 301 SSS 303
D 290 SSS 292

RESULT 13
Q8GS62
ID Q8GS62 PRELIMINARY; PRT; 360 AA.
AC Q8GS62
DT 01-MAR-2003 (TREMREL. 23, Created)
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Cyclin D.
GN CYCD.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Protonema;
RA Lorenz S., Reski R., Decker E.L.;
RT "Cell cycle genes in Physcomitrella patens.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Lorenz S., Reski R., Decker E.L.;
RT "Cell cycle genes in Physcomitrella patens.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ428953; CAD21955.1; -
DR EMBL; AJ488282; CAD32542.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin C; 1.
DR SMART; SM00385; CYCLIN; 1.
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Best Local Similarity 35.1%; Pred. No. 1.3e-32;
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QY 61 DVIYKRLSGDLDLVNGREDALNTWKACEVHQFGPLCFCLANVYLDRLFSLVHDLPSGKG 120
D 67 ADLYERYQSKLSLE-ARLAALEWLKLVHSFYNGPLTVALAVNYMDRLFSRYTFPEGKE 125
QY 121 WTLQILAVACLISLAAKIETEVPMILDLQVGPQFVFEAKSVORMELLVNLKWLRLAI 180
D 126 WMLQLLSVACISLAAKWESDVPILLDFVQEEHIFEAHTIQRMELLVLTLEWRMGV 185
QY 181 TPCSVIRYFLRMKCDQSPSNTLSRSQVIASTTKGIDFLFEPSEAAAVALSVSGE 240
D 186 TPFYSYVDYFFHKLGVSDL-LLRALLSRVSEIILKSIRVTTSLQYLPVVAAASIICALEE 244
QY 241 LQRVHFDN--SFSPLFSLLOKRYKIG-EMIESDGLC-----SQTPN 283
D 245 VTTINTGDLRTFNEL--LVNVESVKDCYIDMRQSEIGPYCVRMGLKRLKHASEPQSPV 302

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QY 284 GVLEV-----SACCFKTHDSSSYT 305
D 303 GVLEAADVSPSGTGLGFSRSPDPVT 330

RESULT 14
Q7XAB6
ID Q7XAB6 PRELIMINARY; PRT; 350 AA.
AC Q7XAB6
DT 01-OCT-2003 (TREMREL. 25, Created)
DT 01-OCT-2003 (TREMREL. 25, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Cyclin D3-1.
GN CYCD3-1.
OS Euphorbia esula (leafy spurge).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbiaceae; Euphorbieae;
OC Euphorbia.
OX NCBI_TaxID=3993;
RN [1]
RP SEQUENCE FROM N.A.
RA Horvath D.P.;
RT "Cloning of cyclin D3 genes from Euphorbia esula.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY340589; AAQ19973.1; -
KW Cyclin.
SQ SEQUENCE 350 AA; 39835 MW; CF080F5E07C6C485 CRC64;

Query Match 25.8%; Score 409; DB 10; Length 350;
Best Local Similarity 34.1%; Pred. No. 9.7e-30;
Matches 115; Conservative 59; Mismatches 91; Indels 72; Gaps 13;

QY 9 SLLCTESVDDDEGMIVDETPISIPQMGFSQSEEEIIMEM 50
D 12 ALYCSSEED-NWSEGVVDIFHEQEDQOGENTSVFPQSSPVDLN-----WEEDELTSVF 62
QY 51 VEKEQHLPSSDYIKRLSGDLDLN---VGRDALNMTWKACEVHQFGPLCFCLANVYL 106
D 63 SKQEQNL-----YKK-----LEINPLAKSRDADVNMKNVNAHVSFTALTSVLAVNVL 112
QY 107 DRFLSVHDLPSGKGWILQILAVACLISLAAKIETEVPMILDLQVGPQFVFEAKSVORME 166
D 113 DRFLSFDLQTEKPMWTLQAVACLSLAKEVETQVPLLDLQVVDYSKYVFEAKTIQRM 172
QY 167 LLVNLKWLRLRAITPCSVIRYFLRMKSKCDQ---EPSNTLSRSQVIASTTKGIDFL 223
D 173 LLVLTSLQWRMNPVPLSFIDYMTRELGLFKDYLCWE---FIRCELIVLSISDMRFIP 228
QY 224 FRPSEAAAVALSVSGELQRVHFDNSFSPLSL--OKERVKKTGEMI----- 270
D 229 YLPFSIAAAILMHVINGIEPSLGDFFE-TQLFGILGIDKEKVNCRMIIELGSRVYGNQ 287
QY 271 ---ESDGLCSQTPNGVLEVSACCFKTHDSSSY 304
D 288 SNKRYKGS--PGSPNCVMDV-----SPSDNSNDWSW 317

RESULT 15
Q9SNV2
ID Q9SNV2 PRELIMINARY; PRT; 330 AA.
AC Q9SNV2
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
DE Cyclin D1.
GN CYCD1.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]

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Search completed: March 23, 2004, 16:39:03
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 16:39:47 ; Search time 61 Seconds
(without alignments)
1426.633 Million cell updates/sec

Title: US-09-530-209A-2
Perfect score: 308
Sequence: 1 MAEENLELLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	207	67.2	287	3 AAG47104	Aag47104 Arabidops
3	207	67.2	308	2 AAY14071	Aay14071 Mitogenic
4	193	62.7	273	3 AAG47105	Aag47105 Arabidops
5	171	55.5	308	3 AAG23337	Aag23337 Arabidops
6	150	48.7	287	3 AAG23338	Aag23338 Arabidops
7	136	44.2	273	3 AAG23339	Aag23339 Arabidops
8	13	4.2	320	3 AAG23790	Aag23790 Arabidops
9	13	4.2	328	3 AAG23789	Aag23789 Arabidops
10	13	4.2	339	3 AAG23788	Aag23788 Arabidops
11	11	3.6	36	6 ABR98363	Abr98363
12	11	3.6	36	7 ADC84709	Adc84709 MCF-7 bre
13	11	3.6	244	6 ABU70573	Abu70573 Human adi
14	11	3.6	295	2 AAR27114	Aar27114 pradi. 3/
15	11	3.6	295	2 AAR29310	Aar29310 Clin D1
16	11	3.6	295	2 AAR44802	Aar44802 Human cyc
17	11	3.6	295	2 AAR54044	Aar54044 bcl-1 pro
18	11	3.6	295	4 AAB90768	Aab90768 Human she
19	11	3.6	295	7 ADE55900	Ade55900 Rat Prote
20	11	3.6	295	7 ADE64090	Ade64090 Rat Prote
21	11	3.6	295	7 ADE55902	Ade55902 Human Pro
22	11	3.6	295	7 ADE55888	Ade55888 Rat Prote
23	11	3.6	295	7 ADE55896	Ade55896 Rat Prote
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25	11	3.6	295	7 ADE64088	Ade64088 Human Pro

26	11	3.6	295	7 ADE55892	Ade55892 Rat Prote
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31	11	3.6	358	3 AAY79322	Aay79322 Maize cyc
32	11	3.6	358	3 AAY79321	Aay79321 Maize cyc
33	11	3.6	358	7 ABR61588	Abr61588 Z. mays c
34	11	3.6	385	5 ABP41466	Abp41466 Human ova
35	11	3.6	618	2 AAW18571	Aaw18571 Human cyc
36	11	3.6	618	2 AAW74572	Aaw74572 Human cyc
37	11	3.6	647	2 AAW00926	Aaw00926 Human cyc
38	11	3.6	647	2 AAW18570	Aaw18570 Human cyc
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ALIGNMENTS

RESULT 1

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ID AAG47103 standard; protein; 308 AA.

XX AC AAG47103;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 59333.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

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Query Match 67.2%; Score 207; DB 3; Length 287;
Best Local Similarity 100.0%; Pred. No. 7.4e-188;
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DB 1 MIVDETPIEISIPQMGFSQSESEIIMEMVEKEKQHLPSDDYIKRLSGDLNVGRDA 60
QY 82 LNWIKACEVHOGFGLCFCLANNYLDRFLSVHDLPSGKMWILQLLAVACLSAAKIEETE 141
DB 61 LNWIKACEVHOGFGLCFCLANNYLDRFLSVHDLPSGKMWILQLLAVACLSAAKIEETE 120
QY 142 VPMLIDLQVGDPQFVFEAKSVQRMELLVNLKWLRLAITPCSYIRYFLRKMSKCDQEPS 201
DB 121 VPMLIDLQVGDPQFVFEAKSVQRMELLVNLKWLRLAITPCSYIRYFLRKMSKCDQEPS 180
QY 202 NTLISRSLOVIASITTKGIDFLFRPSE 228
DB 181 NTLISRSLOVIASITTKGIDFLFRPSE 207

RESULT 3
AAV14071
ID AAV14071 standard; protein; 308 AA.
XX
XX AAY14071;
XX
DT 16-JUL-1999 (first entry)
XX
DE Mitogenic cyclin CYCD4 protein sequence.
XX
KW Mitogenic cyclin; CYCD4; modulator; plant cell cycle; growth inhibitor;
KW plant cell division; cell growth; regulator; cell proliferation;
KW growth regulator; herbicide; cell division progression.
XX
OS Arabidopsis thaliana.
XX
PN WO9922002-A1.
XX
XX 06-MAY-1999.
XX
XX 23-OCT-1998; 98WO-EP006749.
XX
XX 24-OCT-1997; 97EP-00203303.
XX
XX (CROP-) CROPDESIGN NV.
XX
XX Inze D, De Veylder L, De Almeida J;
XX
DR WPI; 1999-312966/26.
XX
XX N-PSDB; AAX36897.
XX
XX DNA sequence encoding a mitogenic cyclin.
XX
PS Claim 1; Page 47-49; 57pp; English.
XX
CC This sequence is the mitogenic cyclin, CYCD4, of the invention. The DNA
CC sequence, vectors containing it, protein encoded by it, or antibodies
CC recognising the protein can be used for modulating plant cell cycle.
```

CC plant cell division and/or growth, for influencing the activity of
 CC mitogenic cyclin in a plant cell, as positive or negative regulator of
 CC cell proliferation, for modifying the growth inhibition caused by
 CC environmental stress conditions, or for use in a screening method for the
 CC identification of inhibitors or activators of cell cycle proteins. A
 CC compound which is an activator or inhibitor of the mitogenic cyclin can
 CC be used as a growth regulator and/or herbicide. The proteins can also be
 CC used to influence cell division progression in yeast, mammals and insects
 XX
 SQ Sequence 308 AA;

Query Match 67.2%; Score 207; DB 2; Length 308;
 Best Local Similarity 99.7%; Pred. No. 7.8e-188;
 Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 DDYIKRLSGDLNVRGRDALNWIWKACEVHGFGLCFCLAMNYLDRFLSVHDLPSGKG 120
 Db 61 DDYIKRLSGDLNVRGRDALNWIWKACEVHGFGLCFCLAMNYLDRFLSVHDLPSGKG 120

QY 121 WILQLLAVACLSLAAKIEETEVPMLIDLQVGPQVFEAKSVQRMELLVNLKWLRLAI 180
 Db 121 WILQLLAVACLSLAAKIEETEVPMLIDLQVGPQVFEAKSVQRMELLVNLKWLRLAI 180

QY 181 TPCSVIRYFLRMKSCDQEPNTLSRSLQVIASTTKGIDFLFRPSPAAAVALSVSGE 240
 Db 181 TPCSVIRYFLRMKSCDQEPNTLSRSLQVIASTTKGIDFLFRPSPAAAVALSVSGE 240

QY 241 LQVHFDNSSFPLSLQKERVKKIGEMIESDGLCSQTPNGVLEVSACCFSPKTHDS 300
 Db 241 LQVHFDNSSFPLSLQKERVKKIGEMIESDGLCSQTPNGVLEVSACCFSPKTHDS 300

QY 301 SSSYTHLS 308
 Db 301 SSSYTHLS 308

RESULT 4

AAG47105
 ID AAG47105 standard; protein; 273 AA.

AC AAG47105;

XX 18-OCT-2000 (first entry)

DT Arabidopsis thaliana protein fragment SEQ ID NO: 59335.

DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS Arabidopsis thaliana.

XX EPI033405-A2.

PN 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

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PR	14-OCT-1999;	99US-0159330P.	PR	16-APR-1999;	99US-0129845P.
PR	14-OCT-1999;	99US-0159331P.	PR	19-APR-1999;	99US-0130077P.
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PR	14-OCT-1999;	99US-0159584P.	PR	23-APR-1999;	99US-0131449P.
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PR	21-OCT-1999;	99US-0160767P.	PR	30-APR-1999;	99US-0132407P.
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PR	26-OCT-1999;	99US-0161359P.	PR	14-MAY-1999;	99US-0134768P.
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QY	156	VFEAKSVQRMELVLN 171	PR	14-JUN-1999;	99US-0139119P.
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XX	XX		PR	18-JUN-1999;	99US-0139457P.
DT	17-OCT-2000 (first entry)		PR	18-JUN-1999;	99US-0139458P.
XX	XX		PR	18-JUN-1999;	99US-0139459P.
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 35503.		PR	18-JUN-1999;	99US-0139460P.
XX	XX		PR	18-JUN-1999;	99US-0139461P.
XX	XX		PR	18-JUN-1999;	99US-0139462P.
KW	Protein identification; signal transduction pathway; metabolic pathway;		PR	18-JUN-1999;	99US-0139463P.
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		PR	18-JUN-1999;	99US-0139750P.
KW	termination sequence.		PR	18-JUN-1999;	99US-0139763P.
XX	XX		PR	18-JUN-1999;	99US-0139817P.
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PN	EP1033405-A2.		PR	23-JUN-1999;	99US-0140354P.
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PD	06-SEP-2000.		PR	24-JUN-1999;	99US-0140823P.
XX	XX		PR	28-JUN-1999;	99US-0140931P.
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PR	28-OCT-1999;	99US-0161920P.
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Query Match 4.2%; Score 13; DB 3; Length 320;		
Best Local Similarity 100.0%; Pred. No. 0.0013;		
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AC	AAG29789;	
XX	17-OCT-2000 (first entry)	
DT	Arabidopsis thaliana protein fragment SEQ ID NO: 35502.	
DE	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	Arabidopsis thaliana.	
OS	Arabidopsis thaliana.	
XX	EP1033405-A2.	
PN	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-00301439.	
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PR	19-APR-1999;	99US-0130077P;
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PR	25-APR-1999;	99US-0130891P;
PR	28-APR-1999;	99US-0131449P;
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Query Match 4.2%; Score 13; DB 3; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACLSLAAK 136
Db 117 QLLAVACLSLAAK 129

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DT 17-OCT-2000 (first entry)
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DE DE
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.

PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.2%; Score 13; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACLSLAAK 136
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Db 128 QLLAVACLSLAAK 140

RESULT 11
ABR98363
ID ABR98363 standard; peptide; 36 AA.
XX
AC ABR98363;
XX
DT 17-SEP-2003 (first entry)
XX
DE Tumour cell growth inhibitor genetic suppressor element peptide SEQ:241.
KW Human; tumour cell growth inhibiting genetic suppressor element;
KW breast cancer; tumour; cytostatic; tumour cell growth inhibitor.
XX
OS Homo sapiens.
XX
PN WO2003008578-A2.
XX
PD 30-JAN-2003.
XX
PF 28-FEB-2002; 2002MO-US006254.
XX
PR 20-JUL-2001; 2001US-0306730P.
XX
PA (UNITI ) UNIV ILLINOIS FOUND.
XX
PI Primiano T, Chang B, Roninson IB;
XX
WPI; 2003-248013/24.
XX
DR Identifying compounds that inhibit mammalian genes necessary for tumor
PT cell growth, useful for inhibiting tumor cell growth, by assaying for
PT expression or activity of several genes necessary for tumor cell growth.
XX
PS Claim 22; Page 67; 145pp; English.
XX
CC The present invention describes a method (M) for identifying a compound
CC (C) that inhibits growth of a mammalian cell. (M) involves culturing a
CC cell in the presence or absence of (C), assaying the cell for expression
CC or activity of one or more enriched genes (see Table 3 in the
CC specification, GI) that have not been previously implicated in cell
CC proliferation, and identifying (C) when expression or activity of at
CC least one of (GI) is lower in presence of (C) than in absence of (C).
CC Also described in a compound (I) that inhibits tumour cell growth and
CC mammalian cell expression or activity of (GI), identified by (M), where
CC (I) is not an inhibitor or RNA synthesis or protein synthesis. (C) and
CC (I) have cytostatic activity and can be used as tumour cell growth
```

CC inhibitors. (M) is useful for identifying a compound that inhibits growth
 CC of a mammalian cell preferably a human tumor cell. (I) is useful for
 CC inhibiting tumor cell growth by inhibiting expression of (G1). (I) is
 CC useful for treating a disease or condition relating to abnormal cell
 CC proliferation or tumor cell growth. ACF18960 to ACF19187 and ABR98351 to
 CC ABR98436 represent sequences used in the exemplification of the present
 CC invention

XX SQ Sequence 36 AA;

Query Match 3.6%; Score 11; DB 6; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
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 Db 25 LAMNYLDRFLS 35

RESULT 12

ADC84709
 ID ADC84709 standard; peptide; 36 AA.

AC ADC84709;

XX 01-JAN-2004 (first entry)

DE MCF-7 breast cancer cell tumor library GSE peptide #13.
 XX cytostatic; cell proliferation; tumor; breast cancer cell;
 KW genetic suppressor element.

XX Homo sapiens.

XX WO2003007884-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-US022868.

XX 20-JUL-2001; 2001US-0306730P.

XX 28-FEB-2002; 2002WO-US006254.

XX (UNII) UNIV ILLINOIS FOUND.

XX Primiano T, Chang B, Roninson IB;

XX WPI; 2003-312622/30.

XX N-PSDB; ADC84837.

XX Identifying compounds that inhibit mammalian genes necessary for tumor
 PT cell growth, useful for inhibiting tumor cell growth, comprises assaying
 PT for expression or activity of several genes necessary for tumor cell
 PT growth.

XX Claim 22; SEQ ID NO 241; 145pp; English.

XX The invention relates to a method of identifying a compound that inhibits
 CC growth of a mammalian cell, comprising culturing a cell in presence or
 CC absence of the compound, assaying the cell for expression or activity of
 CC one or several enriched genes that have not been previously implicated in
 CC cell proliferation, as given in specification, and identifying the
 CC compound when expression or activity of at least one of the enriched
 CC genes is lower in presence of the compound than in its absence. The
 CC method is useful for identifying a compound that inhibits growth of a
 CC mammalian cell preferably a human tumor cell. The compound is useful for
 CC inhibiting tumor cell growth by inhibiting expression of the genes. The
 CC compound is useful for treating a disease or condition relating to
 CC abnormal cell proliferation or tumor cell growth. This sequence
 CC represents a genetic suppressor element (GSE) peptide isolated from the
 CC MCF-7 breast cancer cell tumor library using the method of the invention.

XX SQ Sequence 36 AA;

Query Match 3.6%; Score 11; DB 7; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
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 Db 25 LAMNYLDRFLS 35

RESULT 13

ABU70573
 ID ABU70573 standard; protein; 244 AA.

XX AC ABU70573;

XX 10-JUN-2003 (first entry)

XX Human adipocyte Selected Interacting domain, SID, #204.

XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KW anti-diabetic; protein-protein interaction; diabetes;
 KW yeast 2-hybrid assay; metabolic disorder; obesity.

XX Homo sapiens.

XX WO200286122-A2.

XX 31-OCT-2002.

XX 14-MAR-2002; 2002WO-EP003768.

XX 14-MAR-2001; 2001US-0275734P.

XX (HYBR-) HYBRIGENICS.

XX Legrain P, Daviet L;

XX WPI; 2003-103412/09.

XX N-PSDB; ACA57117.

XX New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 PT obesity or diabetes.

XX Claim 6; Page 173-174; 382pp; English.

XX The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (STM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (STM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (STM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (STM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a
 CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (STM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence represents a SID
 CC (prey) protein of the invention

XX SQ Sequence 244 AA;

Query Match 3.6%; Score 11; DB 6; Length 244;
 Best Local Similarity 100.0%; Pred. No. 0.082; 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 56 LAMNYLDRFLS 66

RESULT 14

AAR271114
 ID AAR27114 standard; protein; 295 AA.

XX AC AAR27114;
 XX 25-MAR-2003 (revised)
 DT 20-MAY-1998 (first entry)
 XX DE pradi.

XX KW Cyclin; embryo; cdc2 protein kinase; parathyroid adenoma; G1;
 KW 11q13/11p15; oncogene; cell cycle regulation.

XX OS Homo sapiens.
 XX PN WO215603-A1.
 XX PD 17-SEP-1992.

XX PF 11-MAR-1992; 92WO-US001925.
 XX PR 11-MAR-1991; 91US-00667711.
 XX PA (GEO) GEN HOSPITAL CORP.

XX PI Arnold A;

XX DR WPI; 1992-331664/40.
 DR N-PSDB; AAQ28889.
 XX PT Prad1 cyclin and DNA encoding it - useful in promoting wound healing,
 PT and for diagnosing and treating cancer.

XX PS Claim 1; Fig 6; 54pp; English.
 XX CC The sequence given is a novel cyclin, pradi. Cyclins are a class of
 CC eukaryotic proteins which are identified by their cyclic accumulation and
 CC destruction at defined points in embryonic cell cycles. They bind to, and
 CC are essential for activation of, cdc2 protein kinase. The PRAD1 mRNA
 CC sequence was isolated from cells of a benign parathyroid adenoma. The
 CC gene was found to map to the 11q13 region and was found to be
 CC overexpressed in those parathyroid adenomas which had a 11q13/11p15
 CC chromosomal rearrangement. The PRAD locus is amplified and expressed in
 CC many squamous cells and mammary carcinomas. PRAD1 is thought to be an
 CC oncogene which figures in a variety of types of neoplasms. PRAD1 mRNA is
 CC highly conserved across species. PRAD1 mRNA levels fluctuate across the
 CC cell cycle, consistent with, but not proving a role in cell cycle
 CC regulation. The peak in PRAD1 mRNA levels occurs late in the cell cycle
 CC or in G1. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 295 AA;

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

RESULT 15

AAR29310

ID AAR29310 standard; protein; 295 AA.

XX AC AAR29310;
 XX 25-MAR-2003 (revised)
 DT 22-APR-1993 (first entry)
 XX DE Cyclin D1 protein.

XX KW Clone; pCYCD1-H12; mutant; yeast; strain; CLN; cyclin; gene; CLN 1;
 KW CLN 2; human; glioblastoma; cDNA library; expression vector; PADNS;
 KW transformant; pCYCD1-21; pCYCD1-19; HeLa.

XX OS Homo sapiens.
 XX PN WO9220796-A2.
 XX PD 26-NOV-1992.

XX PF 18-MAY-1992; 92WO-US004146.
 XX PR 16-MAY-1991; 91US-00701514.
 XX PA (COLD-) COLD SPRING HARBOR LAB.

XX PI Beach DH;
 XX DR WPI; 1992-415774/50.
 DR N-PSDB; AAQ31873.

XX PT Recombinant mammalian D-type cyclin - replaces a CLN-type protein
 PT essential for cell start in budding yeast, its antibodies and probes
 PT being useful in detecting D-type cyclin in biological samples.
 XX PS Claim 6; Fig 2; 75pp; English.

XX CC This sequence is encoded by the clone pCYCD1-H12. A mutant yeast strain
 CC in which two of the three CLN cyclin genes (CLN 1 and CLN 2) were
 CC inactivate and expression of the third was conditional, was used to
 CC identify human cDNA clones that rescue yeast from CLN deficiency. A human
 CC glioblastoma cDNA library carried in a yeast expression vector (PADNS)
 CC was introduced into a mutant yeast strain. Two yeast transformants
 CC (pCYCD1-21 and pCYCD1-19) which grew despite the lack of function of all
 CC three CLN genes and were not revertants, were identified and recovered in
 CC E. coli. These two clones were shown to be independent clone representing
 CC the same gene. A HeLa cDNA library was screened for a full length cDNA
 CC clone using the 1.2 kb insert of pCYCD1-21 as a probe. The sequence
 CC isolated by this method was pCYCD1-H12. This protein has a molecular
 CC weight of approx. 34,000 daltons. Degenerate probes and primers were
 CC designed using the D1 gene sequence. These primers and probes were used
 CC in the isolation of the cyclin D2 and D3 genes. See also AAR29311-12.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 295 AA;

Query Match 3.6%; Score 11; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 0.097;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
 Db 80 LAMNYLDRFLS 90

Search completed: March 23, 2004, 16:46:28
 Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:45:23 ; Search time 24 Seconds

(Without alignments)
662.533 Million cell updates/sec

Title: US-09-530-209A-2

Perfect score: 308

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	4.2	335	4 US-09-404-296B-28	Sequence 28, Appl
2	13	4.2	354	4 US-09-404-296B-2	Sequence 2, Appl
3	11	3.6	102	2 US-08-580-988A-23	Sequence 23, Appl
4	11	3.6	152	2 US-08-460-694-4	Sequence 4, Appl
5	11	3.6	152	3 US-08-460-744-4	Sequence 4, Appl
6	11	3.6	152	3 US-07-667-711B-4	Sequence 4, Appl
7	11	3.6	295	1 US-07-947-120-8	Sequence 8, Appl
8	11	3.6	295	1 US-08-472-893A-8	Sequence 8, Appl
9	11	3.6	295	2 US-08-460-694-2	Sequence 2, Appl
10	11	3.6	295	2 US-08-464-517-2	Sequence 2, Appl
11	11	3.6	295	2 US-08-464-517-19	Sequence 19, Appl
12	11	3.6	295	2 US-08-464-517-20	Sequence 20, Appl
13	11	3.6	295	2 US-08-246-361A-2	Sequence 19, Appl
14	11	3.6	295	2 US-08-246-361A-19	Sequence 19, Appl
15	11	3.6	295	2 US-08-246-361A-20	Sequence 20, Appl
16	11	3.6	295	2 US-08-463-772-2	Sequence 2, Appl
17	11	3.6	295	3 US-08-463-772-19	Sequence 19, Appl
18	11	3.6	295	3 US-08-463-772-20	Sequence 20, Appl
19	11	3.6	295	3 US-08-460-744-2	Sequence 2, Appl
20	11	3.6	295	3 US-07-667-711B-2	Sequence 2, Appl
21	11	3.6	295	3 US-08-947-492-8	Sequence 8, Appl
22	11	3.6	295	5 PCT-US93-05000-2	Sequence 2, Appl
23	11	3.6	295	5 PCT-US93-05000-19	Sequence 19, Appl
24	11	3.6	295	5 PCT-US93-05000-20	Sequence 20, Appl
25	11	3.6	358	4 US-09-398-858-2	Sequence 2, Appl
26	11	3.6	358	4 US-09-398-858-12	Sequence 12, Appl
27	11	3.6	618	2 US-08-770-761A-3	Sequence 3, Appl

28	11	3.6	647	2 US-08-770-761A-8	Sequence 8, Appl
29	11	3.6	660	2 US-08-770-761A-2	Sequence 2, Appl
30	11	3.6	662	2 US-08-770-761A-5	Sequence 5, Appl
31	11	3.6	705	2 US-08-770-761A-7	Sequence 7, Appl
32	11	3.6	819	2 US-08-464-517-7	Sequence 7, Appl
33	11	3.6	819	2 US-08-246-361A-7	Sequence 7, Appl
34	11	3.6	819	2 US-08-463-772-7	Sequence 7, Appl
35	11	3.6	819	5 PCT-US93-05000-7	Sequence 7, Appl
36	10	3.2	189	2 US-08-464-517-21	Sequence 21, Appl
37	10	3.2	189	2 US-08-246-361A-21	Sequence 21, Appl
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39	10	3.2	189	5 PCT-US93-05000-21	Sequence 21, Appl
40	10	3.2	236	2 US-08-464-517-22	Sequence 22, Appl
41	10	3.2	236	2 US-08-246-361A-22	Sequence 22, Appl
42	10	3.2	236	3 US-08-463-772-22	Sequence 22, Appl
43	10	3.2	236	5 PCT-US93-05000-22	Sequence 22, Appl
44	10	3.2	289	2 US-08-246-361A-4	Sequence 4, Appl
45	10	3.2	289	5 PCT-US93-05000-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-09-404-296B-28
; Sequence 28, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-404-296B-2
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Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLAVACTSLAAK 136
Db 128 QLAVACTSLAAK 140

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RESULT 2
US-09-404-296B-2
; Sequence 2, Application US/09404296B
; Patent No. 6559358
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/09/404,296B
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-404-296B-2
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Query Match 4.2%; Score 13; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLAVACTSLAAK 136

Db 142 QLLAVACTSLAAK 154

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RESULT 3
US-08-580-988A-23
; Sequence 23, Application US/08580988A
; Patent No. 5856161
; GENERAL INFORMATION:
; APPLICANT: Aggarwal et al.
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,988A
; FILING DATE: January 3, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5721CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION:
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-580-988A-23

Query Match 3.6%; Score 11; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLS 111
Db 29 LAMNYLDRFLS 39

RESULT 4
US-08-460-694-4
; Sequence 4, Application US/08460694
; Patent No. 585655
; GENERAL INFORMATION:
; APPLICANT: Arnold, Andrew
; TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
```

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STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,694
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McConathy, Evelyn H.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 0609.4070002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-460-694-4

Query Match 3.6%; Score 11; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLS 111
Db 25 LAMNYLDRFLS 35

RESULT 5
US-08-460-744-4
; Sequence 4, Application US/08460744
; Patent No. 6107541
; GENERAL INFORMATION:
; APPLICANT: Arnold, Andrew
; TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,744
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McConathy, Evelyn H.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 0609.4070005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2540
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
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TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-744-4

Query Match 3.6%; Score 11; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFLS 111
DB 25 LANNYLDRFLS 35

RESULT 6
US-07-667-711B-4

; Sequence 4, Application US/07667711B
; Patent No. 610700
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, ANDREW
; TITLE OF INVENTION: Pradl Cyclin and Its CDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/667, 711B
; FILING DATE: 11-MAR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCPHAIL, DONALD R.
; REGISTRATION NUMBER: 35,811
; REFERENCE/DOCKET NUMBER: 0609.4070000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-07-667-711B-4

Query Match 3.6%; Score 11; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFLS 111
DB 25 LANNYLDRFLS 35

RESULT 7
US-07-947-120-8

; Sequence 8, Application US/07947120
; Patent No. 5538846
; GENERAL INFORMATION:
; APPLICANT: Meeker, Timothy C.
; TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and
; TITLE OF INVENTION: Assay Methods
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: Steuart Street Tower, 18th Fl., One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/947,120
; FILING DATE: 19920917
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: 91-210-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-777-9257
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-947-120-8

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFLS 111
DB 80 LANNYLDRFLS 90

RESULT 8
US-08-472-893A-8

; Sequence 8, Application US/08472893A
; Patent No. 5677130
; GENERAL INFORMATION:
; APPLICANT: Meeker, Timothy C.
; TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and
; TITLE OF INVENTION: Assay Methods
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: Steuart Street Tower, 18th Fl., One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,893A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/947,120
; FILING DATE: 17-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: 91-210-1
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-893A-8

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
DB 80 LANMYLDRFLS 90

RESULT 9
US-08-460-694-2
Sequence 2, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConachy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609,4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-694-2

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
DB 80 LANMYLDRFLS 90

RESULT 10
US-08-464-517-2
Sequence 2, Application US/08464517
Patent No. 5869640

GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-517-2

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
DB 80 LANMYLDRFLS 90

RESULT 11
US-08-464-517-19
Sequence 19, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-19

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
|||
DB 80 LAMNYLDRFLS 90

RESULT 12
US-08-464-517-20
Sequence 20, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-517-20

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
|||
DB 80 LAMNYLDRFLS 90

RESULT 13
US-08-246-361A-2
Sequence 2, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-246-361A-2

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111

Db 80 LANVYIDRFLS 90

RESULT 14
US-08-246-361A-19
Sequence 19, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-246-361A-19

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LANVYIDRFLS 111
Db 80 LANVYIDRFLS 90

RESULT 15
US-08-246-361A-20
Sequence 20, Application US/08246361A
Patent No. 5998582
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,361A
FILING DATE: 19-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-246-361A-20

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LANVYIDRFLS 111
Db 80 LANVYIDRFLS 90

Search completed: March 23, 2004, 16:49:05
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:48:19 ; Search time 46 Seconds

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Title: US-09-530-209a-2

Perfect score: 308

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	11	3.6	129	12	US-10-424-599-183234
5	11	3.6	276	15	US-10-116-275-114
6	11	3.6	295	15	US-10-295-027-636
7	11	3.6	323	12	US-10-425-114-38749
8	11	3.6	358	14	US-10-320-230-2
9	11	3.6	358	14	US-10-320-230-12
10	11	3.6	358	15	US-10-409-701-5
11	11	3.6	385	15	US-10-264-049-2598
12	10	3.2	254	9	US-09-778-927A-53
13	10	3.2	289	9	US-09-919-497-54
14	10	3.2	289	13	US-10-024-066-2
15	10	3.2	289	13	US-10-024-066-4

16	10	3.2	349	12	US-10-424-599-178576
17	10	3.2	383	12	US-10-424-599-160824
18	10	3.2	383	12	US-10-424-599-282528
19	10	3.2	427	12	US-10-425-114-38905
20	9	2.9	182	12	US-10-424-599-239678
21	9	2.9	185	12	US-10-424-599-225086
22	9	2.9	238	12	US-10-424-599-273603
23	9	2.9	251	12	US-10-424-599-273602
24	9	2.9	271	12	US-10-424-599-253479
25	9	2.9	309	12	US-10-424-599-218205
26	9	2.9	315	15	US-10-388-269-8
27	9	2.9	340	12	US-10-425-114-49308
28	9	2.9	345	12	US-10-425-114-53407
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37	8	2.6	219	12	US-10-424-599-241697
38	8	2.6	225	15	US-10-369-493-13519
39	8	2.6	229	12	US-10-424-599-226651
40	8	2.6	242	15	US-10-094-749-2076
41	8	2.6	255	12	US-10-424-599-171019
42	8	2.6	291	12	US-10-282-122A-49584
43	8	2.6	292	15	US-10-116-275-275
44	8	2.6	300	14	US-10-141-531-75
45	8	2.6	300	14	US-10-306-292-7

ALIGNMENTS

RESULT 1

US-10-388-269-2 Application US/10388269

Sequence 2, App Publication No. US2003022122A1

GENERAL INFORMATION:

APPLICANT: MURRAY, James Augustus Henry

TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH

FILE REFERENCE: 2121-0151P

CURRENT APPLICATION NUMBER: US/10/388, 269

CURRENT FILING DATE: 2003-03-12

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 354

TYPE: PRT

ORGANISM: Nicotiana tabacum

US-10-388-269-2

Query Match 4.2%; Score 13; DB 15; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR 124 OLAVACLSIAK 136

DB 142 OLAVACLSIAK 154

RESULT 2

US-10-310-154-426

Sequence 426, Application US/10310154

Publication No. US2003033670A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

APPLICANT: Chomel, Paul S.

APPLICANT: Adams, Thomas H

APPLICANT: Ruff, Thomas G.

APPLICANT: Agarwal, Ameeta K.

APPLICANT: Ahrens, Jeffrey E.

```

; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinhua
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshien
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jindong
; APPLICANT: Lu, Bin
; APPLICANT: Luehly, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manohikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Temmeen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanqun
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zhang, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 426
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Zea mays
; US-10-310-154-426

Query Match          3.9%; Score 12; DB 15; Length 349;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      125 LLAVACLSIAAK 136
        |||||
Db      150 LLAVACLSIAAK 161

RESULT 3
US-10-199-820-241
; Sequence 241, Application US/10199820
; Publication No. US20030180739A1
; GENERAL INFORMATION:
; APPLICANT: Board of Trustees of the University of Illinois
; APPLICANT: Primiano, Thomas
; APPLICANT: Chang, Bey-dih
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating Ca
; FILE REFERENCE: 99,216-U
; CURRENT APPLICATION NUMBER: US/10/199,820

```

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; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 241
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-199-820-241

Query Match          3.6%; Score 11; DB 14; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      101 LAMNYDRPLS 111
        |||||
Db      25 LAMNYDRPLS 35

RESULT 4
US-10-424-599-183234
; Sequence 183234, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhao, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 183234
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136474C.1.pcp
; US-10-424-599-183234

Query Match          3.6%; Score 11; DB 12; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      218 GIDFLFRPSE 228
        |||||
Db      9 GIDFLFRPSE 19

RESULT 5
US-10-116-275-114
; Sequence 114, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-116-275-114

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Query Match 3.6%; Score 11; DB 15; Length 276;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYIDRFLS 111
Db 80 LAMNYIDRFLS 90

RESULT 6

US-10-295-027-636
; Sequence 636, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:

APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natsaba
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 636
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-636

Query Match 3.6%; Score 11; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYIDRFLS 111
Db 80 LAMNYIDRFLS 90

RESULT 7

US-10-425-114-38749
; Sequence 38749, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:

APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO: 38749
LENGTH: 323
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73363C10_F11.pap
US-10-425-114-38749

Query Match 3.6%; Score 11; DB 12; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 QLAVACLSLA 134
Db 113 QLAVACLSLA 123

RESULT 8

US-10-320-230-2
; Sequence 2, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
APPLICANT: Lowe, Keith S.
APPLICANT: Tao, Yumin
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gregory, Carolyn A.
APPLICANT: McEliver, John A.
APPLICANT: Hoerster, George J.
TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
FILE REFERENCE: 0926D
CURRENT APPLICATION NUMBER: US/10/320,230
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: 60/101,551
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 09/398,858
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 358
TYPE: PRT
ORGANISM: Zea mays
US-10-320-230-2

Query Match 3.6%; Score 11; DB 14; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 QLAVACLSLA 134
Db 148 QLAVACLSLA 158

RESULT 9

US-10-320-230-12
; Sequence 12, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
APPLICANT: Lowe, Keith S.
APPLICANT: Tao, Yumin

APPLICANT: Gordon-Kamm, William J.
APPLICANT: Gregory, Carolyn A.
APPLICANT: McElvey, John A.
APPLICANT: Hoelster, George J.
TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 0926D
CURRENT APPLICATION NUMBER: US/10/320,230
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: 60/101,551
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 09/398,858
PRIOR FILING DATE: 1999-09-20
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 358
TYPE: PRT
ORGANISM: Zea mays
US-10-320-230-12

Query Match 3.6%; Score 11; DB 14; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACTSLA 134
DB 148 QLLAVACTSLA 158

RESULT 10
US-10-409-701-5
Sequence 5, Application US/10409701
Publication No. US20030221224A1
GENERAL INFORMATION:
APPLICANT: Zinselmeier, Chris
APPLICANT: Helentjaris, Timothy G.
TITLE OF INVENTION: Enhanced Silk Excretion Under Stress
FILE REFERENCE: 1421
CURRENT APPLICATION NUMBER: US/10/409,701
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,796
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 358
TYPE: PRT
ORGANISM: Zea mays
US-10-409-701-5

Query Match 3.6%; Score 11; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACTSLA 134
DB 148 QLLAVACTSLA 158

RESULT 11
US-10-264-049-2598
Sequence 2598, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133PI
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patent In Ver. 3.1
SEQ ID NO 2598
LENGTH: 385
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2598

Query Match 3.6%; Score 11; DB 15; Length 385;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDREPL 111
DB 170 LAMNYLDREPL 180

RESULT 12
US-09-778-927A-53
Sequence 53, Application US/09778927A
Patent No. US20020068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: IL 134453
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL135341
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 53
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(254)
OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-53

Query Match 3.2%; Score 10; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDREPL 110
DB 79 LAMNYLDREPL 88

RESULT 13
US-09-919-497-54
Sequence 54, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 54
LENGTH: 289
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-54

Query Match 3.2%; Score 10; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDREFL 110
Db 79 LAMNYLDREFL 88

RESULT 14
US-10-024-066-2
Sequence 2, Application US/10024066
Publication No. US20020166134A1
GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Pasumarthi, Kishore Babu S.
TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/139,942
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: PCT/US00/16827
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 289
TYPE: PRT
ORGANISM: Mus musculus
US-10-024-066-2

Query Match 3.2%; Score 10; DB 13; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDREFL 110
Db 78 LAMNYLDREFL 87

RESULT 15
US-10-024-066-4
Sequence 4, Application US/10024066
Publication No. US20020166134A1
GENERAL INFORMATION:
APPLICANT: Field, Loren J.
APPLICANT: Pasumarthi, Kishore Babu S.
TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
FILE REFERENCE: 7037-450
CURRENT APPLICATION NUMBER: US/10/024,066
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/139,942
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: PCT/US00/16827
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 289
TYPE: PRT
ORGANISM: Homo sapiens

US-10-024-066-4

Query Match 3.2%; Score 10; DB 13; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDREFL 110
Db 79 LAMNYLDREFL 88

Search completed: March 23, 2004, 16:53:55
Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2004, 16:44:27 ; Search time 21 Seconds

(without alignments)
1410.809 Million cell updates/sec

Title: US-09-530-209A-2

Sequence: 1 MABENLESLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	6.5	317	2	T49995 cyclin protein-lik
2	13	4.2	334	2	S51650 cyclin delta-1 - A
3	13	4.2	339	2	A96725 hypothetical prote
4	12	3.9	291	2	S57922 cyclin D1 - Africa
5	12	3.9	291	2	S62730 cyclin D1 - zebra
6	11	3.6	295	2	A38977 cyclin D1 - human
7	11	3.6	295	2	A56523 cyclin D1 - mouse
8	11	3.6	295	2	JC2342 cyclin D1 - rat
9	11	3.6	418	2	S11678 cyclin A - African
10	10	3.2	288	2	JC4011 cyclin D2 - rat
11	10	3.2	288	2	I58372 cyclin D2 - mouse
12	10	3.2	289	2	A41984 cyclin D2 - human
13	10	3.2	289	2	A42822 cyclin D2 - mouse
14	10	3.2	291	2	JC4579 cyclin D2 - chick
15	9	2.9	291	2	S57925 cyclin D2 - Africa
16	9	2.9	321	2	T04720 hypothetical prote
17	9	2.9	372	2	T09961 cyclin D-like prote
18	9	2.9	376	2	T05420 cyclin delta-3 - A
19	8	2.6	178	2	T28045 hypothetical prote
20	8	2.6	237	2	C40035 cyclin-like protei
21	8	2.6	292	2	T00397 hypothetical prote
22	8	2.6	292	2	B42822 cyclin D3 - human
23	8	2.6	293	2	JC4012 cyclin D3 - rat
24	8	2.6	300	1	A69444 chlorodoxin-disulf
25	8	2.6	302	2	E85041 probable D-type cy
26	8	2.6	318	1	D23766 nodalhecal protein
27	8	2.6	328	2	B83261 hypothetical prote
28	8	2.6	361	2	C84613 probable cyclin D
29	8	2.6	361	2	T45860 cyclin D3-like pro

30	8	2.6	383	2	S51651 cyclin delta-2 - A
31	8	2.6	501	2	T48336 hypothetical prote
32	8	2.6	509	2	S74935 hypothetical prote
33	8	2.6	542	2	S07386 55k protein precu
34	8	2.6	542	2	T35938 probable substrate
35	8	2.6	1383	2	T06091 hypothetical prote
36	8	2.6	1468	2	F70466 RNA polymerase bet
37	7	2.3	62	2	S45295 cyclin Cyc3 - Arab
38	7	2.3	93	2	T01876 hypothetical prote
39	7	2.3	102	2	T35134 hypothetical prote
40	7	2.3	137	2	S03489 T-cell receptor be
41	7	2.3	150	2	G87590 cyclochrome c-type
42	7	2.3	158	2	S61853 hnpk protein - Pae
43	7	2.3	159	2	T04297 hypothetical prote
44	7	2.3	166	2	D75173 hypothetical prote
45	7	2.3	201	1	T29447 probable bacitraci

ALIGNMENTS

RESULT 1

T49995 cyclin protein-lik - Arabidopsis thaliana

N:Alternate names: protein F12B17.210

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C/Accession: T49995

R:Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000

A:Reference number: 225026

A:Accession: T49995

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-317 <BEV>

A:Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.210

A:Experimental source: cultivar Columbia; BAC clone F12B17

C/Genetics:

A:Gene: ATSP:F12B17.210

A:Map position: 5

A:Introns: 78/3; 107/3; 140/3; 221/3; 266/3

Query Match

Best Local Similarity 100.0%; Pred. No. 3.2e-12; Length 317; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 CIANNYIDRPLSVHDLPSGK 119

DB 91 CIANNYIDRPLSVHDLPSGK 110

RESULT 2

S51650 cyclin delta-1 - Arabidopsis thaliana

N:Alternate names: cyclin D homolog

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997

C/Accession: S51650

R:Son, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H. submitted to the EMBL Data Library, December 1994

A:Description: A family of cyclin D homologs from plants differentially controlled by g

A:Reference number: S51650

A:Accession: S51650

A:Molecule type: mRNA

A:Residues: 1-334 <SON>

A:Cross-references: EMBL:X83369; NID:G603504; PID:G603505

C/Keywords: cell cycle control; cell division control

Query Match 4.2%; Score 13; DB 2; Length 334; Best Local Similarity 100.0%; Pred. No. 5.2e-05; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QILAVACISLAK 136

Db 128 QLAVALCTSLAAK 140

RESULT 3

hypothetical protein F20P5.7 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C/Accession: A96725
 R/Rheology: A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 anson, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.R.; Li, J.H.; Liu, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: A96725
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-339 <STO>
 A/Cross-references: GB:AE005173; NID:92194121, PIDN:AA61096.1, GSPDB:GN00141
 C/Genetics:
 A/Gene: F20P5.7
 A/Map position: 1

Query Match 4.2%; Score 13; DB 2; Length 339;
 Best Local Similarity 100.0%; Pred. No. 5.3e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 QLAVALCTSLAAK 136
 128 QLAVALCTSLAAK 140

RESULT 4

cyclin D1 - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
 C/Accession: S57922
 R/Cockerill, M.J.; Hunt, T.
 submitted to the EMBL Data Library, July 1995
 A/Description: D-type cyclins in Xenopus laevis.
 A/Reference number: S57922
 A/Accession: S57922
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-291 <COC>
 A/Cross-references: EMBL:X89475; NID:9897818; PIDN:CAA61664.1; PID:9897819
 C/Superfamily: cyclin
 C/Keywords: cell cycle control

Query Match 3.9%; Score 12; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLSV 112
 78 LAMNYLDRFLSV 89

RESULT 5

662730
 cyclin D1 - zebra fish
 C/Species: Brachydanio rerio (zebra fish)
 C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S62730
 R/Yarden, A.; Salomon, D.; Geiger, B.

Biochim. Biophys. Acta 1264, 257-260, 1995
 A/Title: Zebrafish cyclin D1 is differentially expressed during early embryogenesis.
 A/Reference number: S62730; MUID:96138542; PMID:8547308
 A/Accession: S62730
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-291 <YAR>
 A/Cross-references: EMBL:X87581; NID:91143440; PIDN:CAA60885.1; PID:91143441
 C/Note: the source is designated as Danio rerio
 C/Superfamily: cyclin

Query Match 3.9%; Score 12; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 LAMNYLDRFLSV 112
 Db 80 LAMNYLDRFLSV 91

RESULT 6

cyclin D1 - human
 N/Alternate names: cyclin BCL1; cyclin D; PRAD1; probable bcl-1 transforming protein
 C/Species: Homo sapiens (man)
 C/Date: 27-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 16-Jul-1999
 C/Accession: A38977; A41523; S14794; A40034; B40268; S51701; S54082; S34295
 R/Rimokh, R.; Berger, F.; Baetard, C.; Klein, B.; French, M.; Archimbaud, E.; Rouault,
 Blood 83, 3689-3696, 1994
 A/Title: Rearrangement of CCND1 (BCL1/PRAD1) 3' untranslated region in mantle-cell lymphoma.
 A/Reference number: A38977; MUID:94264323; PMID:8204893
 A/Accession: A38977
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-295 <RIM>
 A/Cross-references: GB:Z23022; NID:9312911; PIDN:CAA60558.1; PID:9312912
 R/Witthers, D.A.; Harvey, R.C.; Faust, J.B.; Melnyk, O.; Carey, K.; Meeker, T.C.
 Mol. Cell. Biol. 11, 4846-4853, 1991
 A/Title: Characterization of a candidate bcl-1 gene.
 A/Reference number: A41523; MUID:9201758; PMID:1833629
 A/Accession: A41523
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-295 <WIT>
 A/Cross-references: GB:M73554; NID:9179364; PIDN:AA58392.1; PID:9179365
 R/Motokura, T.; Bloom, T.; Kim, H.G.; Ueppner, H.; Ruderman, J.V.; Kronenberg, H.M.;
 Nature 350, 512-515, 1991
 A/Title: A novel cyclin encoded by a bcl1-linked candidate oncogene.
 A/Reference number: S14794; MUID:91194766; PMID:1826542
 A/Accession: S14794
 A/Molecule type: mRNA
 A/Residues: 1-295 <MOT>
 A/Cross-references: EMBL:X59798; NID:935631; PIDN:CAA42470.1; PID:935632
 R/Xiong, Y.; Connolly, T.; Fletcher, B.; Beach, D.
 Cell 65, 691-699, 1991
 A/Title: Human D-type cyclin.
 A/Reference number: A40034; MUID:91235304; PMID:1827756
 A/Accession: A40034
 A/Molecule type: mRNA
 A/Residues: 1-129; 'G', '131-187', 'S', '189-295' <XIO>
 A/Cross-references: GB:M64349; NID:9181244; PIDN:AA52136.1; PID:9181245
 A/Note: the authors translated the codon TCT for residue 188 as Leu
 R/Lew, D.J.; Dulic, V.; Reed, S.I.
 Cell 66, 1197-1206, 1991
 A/Title: Isolation of three novel human cyclins by rescue of G1 cyclin (Cln) function
 A/Reference number: A40268; MUID:92005671; PMID:1833066
 A/Accession: B40268
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-167; 'TA', '170-295' <LEW>
 A/Cross-references: GB:M74092
 R/Alberti, S.; Stella, M.; Dell'Arciprete, R.; Bucci, C.; Nutini, M.; Naglieri, A.M.;
 submitted to the EMBL Data Library, February 1994

A;Reference number: S51700
A;Accession: S51701
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 171-295 <ALB>
A;Cross-references: EMBL:X77754
R;Motoyura, T.; Arnold, A.
Genes Chromosomes Cancer 7, 89-95, 1993
A;Title: The PRAD1/cyclin D1 proto-oncogene: Genomic organization, 5' DNA sequence, and
A;Reference number: 154082; MUID:93326527; PMID:7687458
A;Accession: 154082
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-66 <RES>
A;Cross-references: GB:I09054; NID:g307344; PIDN:AAA36481.1; PID:g307345
C;Genetics:
A;Gene: GDB:CCND1; PRAD1; D11528
A;Cross-references: GDB:128222; OMIM:168461
A;Map position: 11q13.1-11q13.1
A;Note: this gene either contains or is contiguous to GDB:BCL1
C;Superfamily: cyclin
C;Keywords: cell cycle control; proto-oncogene

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
Db 80 LANMYLDRFLS 90

RESULT 7
A;Accession: A56523
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1995
C;Accession: A56523; A40035
R;Smith, R.; Peters, G.; Dickson, C.
Genomics 25, 85-92, 1995
A;Title: Genomic organization of the mouse cyclin D1 gene (Cyl-1).
A;Reference number: A56523; MUID:95293413; PMID:7774959
A;Accession: A56523
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-295 <SMT>
A;Cross-references: GB:S78355; NID:g994896; PIDN:AA34495.1; PID:g994897
R;Matsushima, H.; Roussel, M.F.; Ashmun, R.A.; Sherr, C.J.
Cell 65, 701-713, 1991
A;Title: Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the
A;Reference number: A40035; MUID:91233305; PMID:1827757
A;Accession: A40035
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <MAT>
A;Cross-references: GB:M64403; NID:g192877; PIDN:AAA37502.1; PID:g192878
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
Db 80 LANMYLDRFLS 90

RESULT 8
JC2342
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1995

C;Accession: JC2342; S44147
R;Bianchi, S.; Fabiani, S.; Muratori, M.; Arnold, A.; Sakaguchi, K.; Miki, T.; Brandi,
Biochem. Biophys. Res. Commun. 204, 691-700, 1994
A;Title: Calcium modulates the cyclin D1 expression in a rat parathyroid cell line.
A;Reference number: JC2342; MUID:95071382; PMID:7980531
A;Accession: JC2342
A;Molecule type: mRNA
A;Residues: 1-295 <BIA>
A;Cross-references: EMBL:X75207; NID:g473122; PIDN:CAA53020.1; PID:g473123
A;Experimental source: epithelial parathyroid cell line
R;Bianchi, S.; Fabiani, S.; Muratori, M.; Sakaguchi, K.; Arnold, A.; Miki, T.; Brandi,
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and calcium regulation of cyclin D1 gene in a rat parathyroid c
A;Reference number: S44147
A;Accession: S44147
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-295 <B12>
A;Cross-references: EMBL:X75207; NID:g473122; PIDN:CAA53020.1; PID:g473123
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.6%; Score 11; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
Db 80 LANMYLDRFLS 90

RESULT 9
S11678
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1995
C;Accession: S11678
R;Kinshtul, U.; Golsteyn, R.; Hill, C.S.; Hunt, T.
EMBO J. 9, 2865-2875, 1990
A;Title: The A- and B-type cyclin associated cdc2 kinases in Xenopus turn on and off a
A;Reference number: S11678; MUID:90360999; PMID:2143983
A;Accession: S11678
A;Molecule type: mRNA
A;Residues: 1-418 <MIN>
A;Cross-references: EMBL:X53745; NID:g64644; PIDN:CAA37775.1; PID:g64645
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.6%; Score 11; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANMYLDRFLS 111
Db 220 LANMYLDRFLS 230

RESULT 10
JC4011
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Jun-2000
C;Accession: JC4011
R;Hosokawa, Y.; Ohga, T.; Nakashima, K.
Gene 147, 249-252, 1994
A;Title: Induction of D2 and D3 cyclin-encoding genes during promotion of the G1/S tran
A;Reference number: JC4011; MUID:95011623; PMID:7926809
A;Accession: JC4011
A;Molecule type: mRNA
A;Residues: 1-288 <HOS>
A;Cross-references: GB:D16308; NID:g577334; PIDN:BA03815.1; PID:g577335
A;Experimental source: Nb2 cell
A;Note: The authors translated the codon GAA for residue 68 as Glu, TGC for residue 104

C;Genetics:
A;Gene: d2
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 11
158372
cyclin D2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 158372
R;Hanna, Z.; Jankowski, M.; Tremblay, P.; Jiang, X.M.; Malatovich, A.; Francke, U.; Jolh
Oncogene 8, 1661-1666, 1993
A;Title: The YIN1 gene, identified by provirus insertional mutagenesis, is the cyclin D2
A;Reference number: 158372; MUID:93275661; PMID:8502486
A;Accession: 158372
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-288 <RES>
A;Cross-references: GB:109752; NID:g203703; PIDN:AAA41010.1; PID:g203704
C;Genetics:
A;Gene: YIN1
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 12
A41964
cyclin D2 - mouse
N;Alternate names: cyclin-like protein Cy12
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A41964; B40035
R;Kiyokawa, H.; Busquets, X.; Powell, C.T.; Ngo, L.; Rikkind, R.A.; Marks, P.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2444-2447, 1992
A;Title: Cloning of a D-type cyclin from murine erythroleukemia cells.
A;Reference number: A41964; MUID:92196134; PMID:1372445
A;Accession: A41964
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-289 <KIT>
A;Cross-references: GB:M63749; NID:G192938; PIDN:AAA37519.1; PID:G192939
A;Experimental source: erythroleukemia cells
A;Note: sequence extracted from NCBI backbone (NCBIN:88492, NCBI:88493)
R;Matsumine, H.; Rousset, M.F.; Ashmun, R.A.; Sherr, C.J.
Cell 65, 701-713, 1991
A;Title: Colony-stimulating factor 1 regulates novel cyclins during the G1 phase of the
A;Reference number: A40035; MUID:91235305; PMID:1827757
A;Accession: B40035
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 54-289 <MAT>
A;Cross-references: GB:M66182
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 13
A42822
cyclin D2 - human
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A42822; I37268; A42821; S26580
R;Xiong, Y.; Menninger, J.; Beach, D.C.
Genomics 13, 575-584, 1992
A;Title: Molecular cloning and chromosomal mapping of CCND genes encoding human D-type
A;Reference number: A42822; MUID:92347851; PMID:1386336
A;Accession: A42822
A;Molecule type: mRNA
A;Residues: 1-289 <XIO>
A;Cross-references: GB:M90813; NID:G179999; PIDN:AAA51926.1; PID:G180000
A;Note: sequence extracted from NCBI backbone (NCBIN:109683, NCBI:109685)
R;Palmero, I.; Holder, A.; Sinclair, A.J.; Dickson, C.; Peters, G.
Oncogene 8, 1049-1054, 1993
A;Title: Cyclins D1 and D2 are differentially expressed in human B-lymphoid cell lines
A;Reference number: I37268; MUID:93205384; PMID:8455931
A;Accession: I37268
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-289 <RE2>
A;Cross-references: EMBL:X68452; NID:G38415; PIDN:CAA48493.1; PID:G38416
R;Inaba, T.; Matsumine, H.; Valentine, M.; Rousset, M.F.; Sherr, C.J.; Look, A.T.
Genomics 13, 565-574, 1992
A;Title: Genomic organization, chromosomal localization, and independent expression of
A;Reference number: A42821; MUID:92347850; PMID:1386335
A;Accession: A42821
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-165; 'NV', 168-223; 'H', 225-240 <RES>
A;Cross-references: GB:M88083; NID:G180008; PIDN:AAA51928.1; PID:G180010
C;Genetics:
A;Gene: GDB:CCND2
A;Cross-references: GDB:128968; OMIM:123833
A;Map position: 12p13-12p13
C;Superfamily: cyclin
C;Keywords: cell cycle control

Query Match 3.2%; Score 10; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFL 110
Db 79 LAMNYLDRFL 88

RESULT 14
JC4579
cyclin D2 - chicken
N;Alternate names: Cy1 D2
C;Species: Gallus gallus (chicken)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 31-Mar-2000
C;Accession: JC4579
R;Li, H.; Grenet, J.; Kidd, V.J.
Gene 167, 341-342, 1995
A;Title: Structure and gene expression of avian cyclin D2.
A;Reference number: JC4579; MUID:96144302; PMID:8566807
A;Accession: JC4579
A;Molecule type: mRNA
A;Residues: 1-291 <LIH>

A/Cross-references: GB:U28980; NID:g968968; PIDN:AA6955.1; PID:g968968
A/Experimental source: U93 T-cell
C/Comment: This protein acts as a regulator of the cell-cycle-dependent protein kinase gene product, binds to these products in a combinatorial fashion, activates their enzyme activity
C/Genetics:
A/Gene: cycl2
C/Superfamily: cyclin
C/Keywords: cell cycle control
F/29-193/Region: cyclin-box similarity

Query Match 3.2%; Score 10; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFL 110
|||
Db 79 LAMNYIDRFL 88

RESULT 15

S57925
cyclin D2 - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Jan-1996 #sequence_rev10n 12-Apr-1996 #ext_change 16-Jul-1999
C/Accession: S57925; S51681
R/Cockerill, M.J.; Hunt, T.
submitted to the EMBL Data Library, July 1995
A/Description: D-type cyclins in Xenopus laevis.
A/Reference number: S57922
A/Accession: S57925
A/Molecule type: mRNA
A/Residues: 1-291 <COC>
A/Cross-references: EMBL:X89476; NID:g897820; PIDN:CAA61665.1; PID:g897821
R/Raib, F.; Jesus, C.
submitted to the EMBL Data Library, December 1994
A/Reference number: S51681
A/Accession: S51681
A/Molecule type: mRNA
A/Residues: 1-291 <RAI>
A/Cross-references: EMBL:X83503; NID:g603899; PIDN:CAA58493.1; PID:g603900
C/Superfamily: cyclin
C/Keywords: cell cycle control

Query Match 2.9%; Score 9; DB 2; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 AMNYIDRFL 110
|||
Db 80 AMNYIDRFL 88

Search completed: March 23, 2004, 16:48:29
Job time: 23 secs

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OM protein - protein search, using SW model

Run on: March 23, 2004, 16:40:35 ; Search time 18 Seconds
(without alignments)
890,978 Million cell updates/sec

Title: US-09-530-209a-2

Perfect score: 308
Sequence: 1 MAEENIEISLCTESNVDE.....SACCFSEKTHDSSSYHLIS 308

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : SwissProt_42.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	4.2	335	1 CGD1_ARATH	P42751 arabidopsis
2	12	3.9	291	1 CGD1_BRARE	O90459 brachydanio
3	12	3.9	291	1 CGD1_XENLA	P50785 xenopus lae
4	11	3.6	292	1 CGD1_CHICK	P55189 gallus gall
5	11	3.6	295	1 CGD1_HUMAN	P24385 homo sapien
6	11	3.6	295	1 CGD1_MOUSE	P25342 mus musculu
7	11	3.6	295	1 CGD1_MOUSE	P39948 rattus norv
8	11	3.6	418	1 CGA1_XENLA	P18606 xenopus lae
9	10	3.2	288	1 CGD2_RAT	O04897 rattus norv
10	10	3.2	289	1 CGD2_HUMAN	P30279 homo sapien
11	10	3.2	289	1 CGD2_MOUSE	P30280 mus musculu
12	10	3.2	291	1 CGD2_CHICK	P49706 gallus gall
13	9	2.9	291	1 CGD2_XENLA	P53782 xenopus lae
14	9	2.9	376	1 CGD3_ARATH	P42753 arabidopsis
15	8	2.6	292	1 CGD3_HUMAN	P30281 homo sapien
16	8	2.6	292	1 CGD3_MOUSE	P30282 mus musculu
17	8	2.6	293	1 CGD3_RAT	P48961 rattus norv
18	8	2.6	318	1 MODD_RHILT	P04680 rhizobium 1
19	8	2.6	361	1 CGD2_ARATH	P42752 arabidopsis
20	8	2.6	382	1 CGD2_ORYSA	O94939 oryza sativ
21	8	2.6	391	1 CGA1_CARAU	O92161 carassius a
22	8	2.6	542	1 XPS5_STRUT	P06109 streptomyce
23	8	2.6	1375	1 RPOB_COXBU	O87903 coxiella bu
24	8	2.6	1468	1 RPOB_AOVAE	O67762 aquilex aeo
25	7	2.3	104	1 GLRX_VERFO	O81187 veronica fo
26	7	2.3	124	1 PHPI_MOUSE	O9dak9 mus musculu
27	7	2.3	220	1 REHY_ORYSA	P52573 oryza sativ
28	7	2.3	233	1 B915_XENLA	P40745 xenopus lae
29	7	2.3	240	1 ATP7_ARATH	O96j12 arabidopsis
30	7	2.3	244	1 FIMB_BOAPE	P33409 bordetella
31	7	2.3	246	1 PHBB_CHMVI	P45335 chromatinum
32	7	2.3	251	1 GLO2_BUCAI	P57336 buchnera ap
33	7	2.3	251	1 Y137_CHLUPN	O92946 chlamydia p

34	7	2.3	253	1	UT11_MOUSE	O9czj1 mus musculu
35	7	2.3	277	1	THIG_SYNEL	O8dmp6 synechococ
36	7	2.3	279	1	MOVP_CMYIX	O66119 cucurbit mo
37	7	2.3	309	1	PANC_MYCTU	O06280 mycobacteri
38	7	2.3	333	1	AMP_TMBPA	O24006 i antimicro
39	7	2.3	394	1	MPGS_AERPE	O9ydm5 aeropyrum p
40	7	2.3	395	1	Y063_SYNY3	O55147 synechocyc
41	7	2.3	424	1	CRIC_ORYSA	O96148 oryza sativ
42	7	2.3	428	1	CG2B_ARATH	P30183 arabidopsis
43	7	2.3	444	1	RBL_MATAN	P93936 watsomla an
44	7	2.3	462	1	ALB3_ARATH	O8lbp4 arabidopsis
45	7	2.3	467	1	ROCE_BACST	P39137 bacillus su

ALIGNMENTS

RESULT 1
CGD1_ARATH STANDARD; PRT; 335 AA.
AC P42751; O04525;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cyclin delta-1.
GN CYCD1 OR AT1G70210 OR F20P5.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
RT by growth regulators and containing the conserved retinoblastoma
RT protein interaction motif."
RL Plant Cell 7:85-103(1995).
RN [2]
RP REVISIONS.
RA Murray J.A.H.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Becker U.R., Palm C.U., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brookes S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetskaia I., Kutz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Maltischer J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.O., Tambunga G., Tortum M.O., Town C.D.,
RA Utechtack T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:81-820(2000).
RN [4]
RP SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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CC EMBL; X83369; CAA58285.1; -.
 CC EMBL; AC002062; AAB61096.1; -.
 DR PIR; A96725; A96725.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR CYCLIN; Cell cycle; Cell division; Multigene family.
 FT CONFLICT 313 313 S -> SPSSS (IN REF. 3).
 SQ SEQUENCE 335 AA; 37868 MW; D365673D2FC639 CRC64;

Query Match 4.2%; Score 13; DB 1; Length 335;
 Best Local Similarity 100.0%; Pred. No. 0.0001;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLAVALCTSLAAK 136
 DB 128 QLAVALCTSLAAK 140

RESULT 2
 ID CGDI_BRARE STANDARD; PRT; 291 AA.
 AC Q80459;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE GI/S-specific cyclin D1.
 GN CCND1 OR CYCD1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96138542; PubMed=8547308;
 RA Yarden A.; Salomon D.; Geiger B.;
 RT "Zebrafish cyclin D1 is differentially expressed during early
 embryogenesis.";
 RU Biochim. Biophys. Acta 1264:257-260(1995).
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 impacts substrate specificity to the complex.
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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CC EMBL; X87581; CAA60885.1; -.
 DR PIR; S62730; S62730.
 DR ZFIN; ZDB-GENE-980526-176; ccnd1.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.

KW Cyclin; Cell cycle; Cell division.
 SQ SEQUENCE 291 AA; 33067 MW; FA5274CB1B46D5EF CRC64;

Query Match 3.9%; Score 12; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00084;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFLSV 112
 DB 80 LAMNYIDRFLSV 91

RESULT 3
 ID CGDI_XENLA STANDARD; PRT; 291 AA.
 AC P50755;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE GI/S-specific cyclin D1.
 GN CCND1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cockerill M.J.; Hunt T.;
 RU Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 impacts substrate specificity to the complex.
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.

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CC EMBL; X89475; CAA61664.1; -.
 DR PIR; S57922; S57922.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;

Query Match 3.9%; Score 12; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.00084;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYIDRFLSV 112
 DB 78 LAMNYIDRFLSV 89

RESULT 4
 ID CGDI_CHICK STANDARD; PRT; 292 AA.
 AC P55169;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE G1/S-specific cyclin D1.
 GN CCND1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OK NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li H., Lahti J.M., Kidd V.J.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition. Interacts with the CDK4 and CDK6 protein
 CC kinases (by similarity).
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC -----
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 CC -----
 DR EMBL: U40844; AAA83271.1; -
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; cyclin_1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 KW CYCLIN; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;
 Query Match 3.6%; Score 11; DB 1; Length 292;
 Best Local Similarity 100.0%; Pred. No. 0.0078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 LAMNYLDRPLS 111
 DB 80 LAMNYLDRPLS 90
 CG1 HUMAN STANDARD; PRT; 295 AA.
 ID CGD1 HUMAN
 AC P24385;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G1/S-specific cyclin D1 (PRAD1 oncogene) (BC1-1 oncogene).
 GN CCND1 OR PRAD1 OR BCL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91194766; PubMed=1826542;
 RA Motokura T., Bloom T., Kim H.G., Ueppner H., Ruderman J.V.,
 RA Kronenberg H.M., Arnold A.;
 RT "A novel cyclin encoded by a bcl1-linked candidate oncogene";
 RL Nature 350:512-515(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92005671; PubMed=1833066;
 RA Lew D.J., Dulic V., Reed S.I.;
 RT "Isolation of three novel human cyclins by rescue of G1 cyclin (Cln)
 function in yeast";
 RL Cell 66:1197-1206(1991).
 RN [3]
 RP SEQUENCE FROM N.A.

RX MEDLINE=91235304; PubMed=1827756;
 RA Xiong Y., Connolly T., Fitchner B., Beach D.;
 RT "Human D-type cyclin";
 RL Cell 65:691-699(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92017758; PubMed=1833629;
 RA Withers D.A., Harvey R.C., Faust J.B., Melnyk O., Carey K.,
 RA Wecker T.C.;
 RT "Characterization of a candidate bcl-1 gene";
 RL Mol. Cell. Biol. 11:4846-4853(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94264323; PubMed=8204893;
 RA Rimokh R., Berger F., Bastard C., Klein B., French M., Archimbaud E.,
 RA Rouault J.-P., Santa Lucia B., Duret L., Vulliamme M.;
 RT "Rearrangement of CCND1 (BCL1/PRAD1) 3' untranslated region in
 RT mantle-cell lymphomas and t(11q13)-associated leukemias";
 RL Blood 83:3689-3696(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wittrik L.A., Nickerson D.A.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Helen F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Maltby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hully S.W.,
 RA Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP INTERACTION WITH CDK4 AND CDK6
 RX MEDLINE=94134440; PubMed=8302605;
 RA Bates S., Bonetta L., McAllian D., Parry D., Holder A., Dickson C.,
 RA Peters G.;
 RT "CDK6 (PLSTIRE) and CDK4 (PSK-T3) are a distinct subset of the
 RT cyclin-dependent kinases that associate with cyclin D1";
 RL Oncogene 9:71-79(1994).
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 CC (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
 CC imparts substrate specificity to the complex.
 CC -1- DISBASE: Involved in B-lymphocytic malignancy (particularly
 CC mantle-cell lymphoma (MCL)) by a chromosomal translocation
 CC t(11;14)(q13;q32) that involves CCND1 and immunoglobulin gene
 CC regions (BCL1 oncogene). Activation of CCND1 may be oncogenic by
 CC directly altering progression through the cell cycle.
 CC -1- DISBASE: Involved in a subset of parathyroid adenomas by a
 CC chromosomal translocation t(11;11)(q13;p15) that involves CCND1
 CC and the parathyroid hormone (PTH) enhancer (PRAD1 oncogene).
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BCL1.html".

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CC -----
DR EMBL; X59798; CAA42470.1; -
DR EMBL; M74092; -; NOT ANNOTATED_CDS.
DR EMBL; M64349; AAA52136.1; -
DR EMBL; M73554; AAA58392.1; -
DR EMBL; Z23022; CAA80558.1; -
DR EMBL; AF511593; AAA43300.2; -
DR EMBL; BC000076; AAH00076.1; -
DR EMBL; BC001501; AAH01501.1; -
DR EMBL; BC014078; AAH14078.1; -
DR EMBL; BC023620; AAH23620.1; -
DR EMBL; BC025302; AAH25302.1; -
DR PIR; A38977; A38977.
DR Genew; HGNC:1582; CCND1.
DR GK; P24385; -
DR MIM; 151400; -
DR MIM; 168461; -
DR GO; GO:0000082; P:G1/S transition of mitotic cell cycle; NMS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C_1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene;
KW Chromosomal translocation.
FT CONFLICT 130 130 N -> G (IN REF. 3).
FT CONFLICT 168 169 MP -> IA (IN REF. 2).
FT CONFLICT 188 188 L -> S (IN REF. 3).
SQ SEQUENCE 295 AA; 33729 MW; 3CC00C905F58D3A CRC64;

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
DB 80 LAMNYLDRFLS 90

RESULT 6
CGDI MOUSE STANDARD; PRT; 295 AA.
ID CGDI_MOUSE
AC P25322;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE G1/S-specific cyclin D1.
GN CCND1 OR CYL-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91235305; PubMed=1827757;
RA Macintosh H., Rousset M.F., Ashmun R.A., Sherr C.J.;
RT "Colony-stimulating factor 1 regulates novel cyclins during the G1
RT phase of the cell cycle.";
RL Cell 65:701-713(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95293413; PubMed=7774959;
RA Smith R., Peters G., Dickson C.;

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RT "Genomic organization of the mouse cyclin D1 gene (Cyl-1).";
RL Genomics 25:85-92(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Hopkins S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopskins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Strapleno M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehlyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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CC -----
DR EMBL; M64403; AAA37502.1; -
DR EMBL; S78355; AAB34495.1; -
DR EMBL; BC044841; AAR44841.1; -
DR PIR; A56523; A56523.
DR MGD; MGI:88313; Ccnd1.
DR GO; GO:0005829; C:cytosol; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0016538; F:cyclin-dependent protein kinase, intrinsic . . . IDA.
DR GO; GO:0045444; F:adipocyte differentiation; IDA.
DR GO; GO:0000320; P:entry into mitotic cell cycle; IDA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C_1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
KW Cyclin;
SQ SEQUENCE 295 AA; 33428 MW; 3A7973684163251B CRC64;

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRFLS 111
DB 80 LAMNYLDRFLS 90

RESULT 7
CGDI RAT STANDARD; PRT; 295 AA.
ID CGDI_RAT

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AC P39948; (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE G1/S-specific cyclin D1.
GN CCND1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93330551; PubMed=8336937;
RA Tamura K., Kaneko Y., Jinno S., Nagata A., Ogiso Y., Shimizu K.,
RA Hayakawa T., Nojima H., Okayama H.;
RT "Cyclin G: a new mammalian cyclin with homology to fission yeast
RT Cig1."
RL Oncogene 8:2113-2118(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95071382; PubMed=7980531;
RA Bianchi S., Fabiani S., Muratori M., Arnold A., Sakaguchi K., Miki T.,
RA Brandi M.L.;
RT "Calcium modulates the cyclin D1 expression in a rat parathyroid cell
RT line."
RL Biochem. Biophys. Res. Commun. 204:691-700(1994).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition. Interacts with the CDK4 and CDK6 protein
CC kinases.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
DR EMBL; D14014; BAA03115.1; -
DR EMBL; X75207; CAA53020.1; -
DR PIR; JC2342; JC2342.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00384; cyclin; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
FT CONFLICT 25 DRV -> RPD (IN REF. 1).
SQ SEQUENCE 295 AA; 33482 MW; C777436B5C79635E CRC64;

Query Match 3.6%; Score 11; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYDRPLS 111
DB 80 LAMNYDRPLS 90

RESULT 8
CGAL_XENIA STANDARD; PRT; 418 AA.
ID CGAL_XENIA
AC P18606;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclin A1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=90360999; PubMed=2143983;
RA Minshull J., Colesteyn R., Hill C.S., Hunt T.;
RT "The A- and B-type cyclin associated cdc2 kinases in Xenopus turn on
RT and off at different times in the cell cycle."
RL EMBO J. 9:2865-2875(1990).
CC -1- FUNCTION: May be involved in the control of the cell cycle at the
CC G1/S (start) and G2/M (mitosis) transitions (By similarity).
CC -1- SUBUNIT: Interacts with the CDK2 and the CD2 protein kinases to
CC form a serine/threonine kinase holoenzyme complex. The cyclin
CC subunit imparts substrate specificity to the complex (By
CC similarity).
CC -1- DEVELOPMENTAL STAGE: Present in eggs and early embryos but cannot
CC be detected in late embryos.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin A2 subfamily.
CC -----
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CC -----
DR EMBL; X53745; CAA37775.1; -
DR PIR; S11678; S11678.
DR HSSP; P30274; IVIN.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00384; cyclin; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
SQ SEQUENCE 418 AA; 46772 MW; FEA0B7A1F0D11B6A CRC64;

Query Match 3.6%; Score 11; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYDRPLS 111
DB 220 LAMNYDRPLS 230

RESULT 9
CGD2_RAT STANDARD; PRT; 288 AA.
ID CGD2_RAT
AC Q04837;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE G1/S-specific cyclin D2 (Vin-1 proto-oncogene).
GN CCND2 OR VIN-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93275661; PubMed=8502486;
RA Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,
RA Franke U., Jolicoeur P.;
RT "The Vin-1 gene, identified by provirus insertional mutagenesis, is
RT the cyclin D2."
RL Oncogene 8:1661-1666(1993).
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE=95011623; PubMed=7926809;
RA Hosokawa Y., Onga T., Nakashima K.;
RT "Induction of D2 and D3 cyclin-encoding genes during promotion of the
RL G1/S transition by prolactin in rat Nb2 cells.";
RL Gene 147:249-252(1994).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
DR EMBL; L09752; AAA41010.1; -
DR EMBL; D16308; BAA03815.1; -
DR PIR; I58372; I58372.
DR PIR; JC4011; JC4011.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLIN; 1.
KM Cyclin, cell cycle, cell division; Multigene family; Proto-oncogene.
FT CONFLICT 68 E -> G (IN REF. 2).
FT CONFLICT 104 C -> V (IN REF. 2).
FT CONFLICT 232 T -> A (IN REF. 2).
SQ SEQUENCE 288 AA; 32826 MW; 4B522BFA935FC1 CRC64;

Query Match 3.2%; Score 10; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 101 LAMNYLDRFL 110
Db 78 LAMNYLDRFL 87

RESULT 10
CGD2 HUMAN STANDARD; PRT; 289 AA.
AC P30279; O13955;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE G1/S-specific cyclin D2.
GN CCND2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92347851; PubMed=1386336;
RA Xiong Y., Menninger J., Beach D., Ward D.C.;
RT "Molecular cloning and chromosomal mapping of CCND genes encoding
RL human D-type cyclins.";
RL Genomics 13:575-584(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93205384; PubMed=8455931;
RA Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;
RT "Cyclins D1 and D2 are differentially expressed in human B-lymphoid
cell lines.";

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RL Oncogene 8:1049-1054(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Miyajima N.;
RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen C.P., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Wiltrik L.A., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=22386257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Hsieh F.,
RA Datchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP SEQUENCE OF 1-240 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92347850; PubMed=1386335;
RA Inaba T., Matsushime H., Valentine M., Roussee M.F., Sherr C.J.,
RA Look A.T.;
RT "Genomic organization, chromosomal localization, and independent
RT expression of human cyclin D genes.";
RL Genomics 13:565-574(1992).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
DR EMBL; M90813; AAA51926.1; -
DR EMBL; X68452; CAA48493.1; -
DR EMBL; D13639; BAA02802.1; -
DR EMBL; AF518005; AAM54041.1; -
DR EMBL; BC010958; AAT10958.1; -
DR EMBL; M88083; AAA51928.1; -
DR EMBL; M88080; AAA51928.1; JOINED.
DR EMBL; M88081; AAA51928.1; JOINED.
DR EMBL; M88082; AAA51928.1; JOINED.
DR PIR; A42822; A42822.
DR Genew; HGNC:1593; CCND2.
DR GK; P30279; -
DR MIM; 123853; -
DR InterPro; IPR006670; Cyclin.

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DR InterPro: IPR004367; Cyclin Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR SMART: SM00384; cyclin_C; 1.
DR SMART: SM00385; CYCLIN_C; 1.
DR PROSITE: PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
FT CONFLICT 166 167 KL -> NV (IN REF. 6).
FT CONFLICT 224 224 T -> H (IN REF. 6).
SQ SEQUENCE 289 AA; 33067 MW; E4E5FEF476D76D90 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 289;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFL 110
DB 79 LANNYLDRFL 88

RESULT 11
CGD2_MOUSE STANDARD; PRT; 289 AA.
AC P30280;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G1/S-specific cyclin D2.
GN CCND2 OR CYL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196134; PubMed=1372445;
RA Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
RA Marks P.A.;
RT "Cloning of a D-type cyclin from murine erythroleukemia cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91235305; PubMed=1827757;
RA Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.;
RT "Colony-stimulating factor 1 regulates novel cyclins during the G1
RT phase of the cell cycle.";
RL Cell 65:701-713(1991).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
CC -----
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CC -----
CC EMBL: M83749; AAA37519.1; -.
CC EMBL: M86182; AAA37503.1; -.
CC PIR: A41984; A41984.
CC MGD: MGI:88314; Ccnd2.
CC GO: GO:0000074; P:regulation of cell cycle; IMP.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN_C; 1.

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DR PROSITE: PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
SQ SEQUENCE 289 AA; 32897 MW; 58F32277DD1DA3D CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 289;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFL 110
DB 78 LANNYLDRFL 87

RESULT 12
CGD2_CHICK STANDARD; PRT; 291 AA.
AC P49706;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G1/S-specific cyclin D2.
GN CCND2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144302; PubMed=8566807;
RA Li H., Grenet J., Kidd V.J.;
RA "Structure and gene expression of avian cyclin D2.";
RL Gene 167:341-342(1995).
CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
CC (start) transition.
CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
CC a serine/threonine kinase holoenzyme complex. The cyclin subunit
CC impacts substrate specificity to the complex.
CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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CC -----
CC EMBL: U28980; AAA69655.1; -.
CC PIR: J04579; J04579.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN_C; 1.
DR PROSITE: PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Multigene family.
SQ SEQUENCE 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 291;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANNYLDRFL 110
DB 79 LANNYLDRFL 88

RESULT 13
CGD2_XENLA STANDARD; PRT; 291 AA.
AC P53782;

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DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D2.
 GN CCND2.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 CC Xenopodidae; Xenopus.
 CC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cockrell M.J., Hunt T.,
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97380591; PubMed=9237366;
 RA Tatabe F., Jeesus C.,
 RT "Xenopus cyclin D2: cloning and expression in oocytes and during
 early development."
 RL Biol. Cell 88:99-111 (1996).
 CC -1- FUNCTION: Essential for the control of the cell cycle at the G1/S
 (start) transition.
 CC -1- SUBUNIT: Interacts with the CDK4 and CDK6 protein kinases to form
 a serine/threonine kinase holoenzyme complex. The cyclin subunit
 imparts substrate specificity to the complex.
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
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 CC -----
 DR EMBL: X89476; CAA61665.1; -;
 DR EMBL: X83503; CAA58493.1; -;
 DR PIR: S57925; S57925.
 DR InterPro: IPR006670; Cyclin.
 DR InterPro: IPR004367; Cyclin_Cterm.
 DR InterPro: IPR006671; Cyclin_N.
 DR Pfam: PF00134; Cyclin; 1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 KM Cyclin; Cell cycle; Cell division; Multigene family.
 SQ SEQUENCE 291 AA; 32959 MW; 9A290F04F1531B89 CRC64;
 Query March 2.9%; Score 9; DB 1; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 102 AMNYLDRFL 110
 |||||
 DB 80 AMNYLDRFL 88
 RESULT 14
 CGD3 ARATH
 ID CGD3 ARATH STANDARD; PRT; 376 AA.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclin delta-3.
 GN CYCD3 OR AT4G34160 OR F28A23.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CC NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta; TISSUE=Seedling;
 RX MEDLINE=95210930; PubMed=7696881;
 RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
 RT "A family of cyclin D homologs from plants differentially controlled
 by growth regulators and containing the conserved retinoblastoma
 protein interaction motif."
 RL Plant Cell 7:85-103 (1995).
 RN [2]
 RP REVISION TO 371.
 RA Murray J.A.H.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Scheller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Srikema W., Ertan K.-D., Terry N.,
 RA Harris B., Anstorge W., Brandt P., Griwell L.A., Rieger M.,
 RA Weissegartner M., de Simone V., Obermaier B., Macne R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohenseil J., Zimmermann W., Medler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA van der Schueren J., Grynoprez B., Chuang Y.-J., Vandenbusche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Kert R., Defoor E.,
 RA Weitzengraber T., Bothe G., Kampberger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berninger S., Hempel S., Feldpausch M., Lambrecht S., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
 RA Pettit A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Blecker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argirou A., Vitale D., Liguori R., Pirvadi E.,
 RA Massenet O., Quigley F., Clabaud G., Muehlen A., Felber R.,
 RA Schindl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chefor F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Glibons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielke C.,
 RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latorille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mink P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hiller L.W.,
 RA Nelson J., Splich U., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drome K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Saby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shondy N., Haegawa A., Hameed A., Lochi M., Johnson A.,
 RA Chen E., Marra M.A., Martienssen R., McComble W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana."
 RL Nature 402:769-777 (1999).
 CC -1- SIMILARITY: Belongs to the cyclin family. Cyclin D subfamily.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X83371; CAA58287.1; -;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 23, 2004, 16:43:48 ; Search time 45 Seconds
(without alignments)
2159.547 Million cell updates/sec

Title: US-09-530-209a-2

Sequence: 1 MAEENLESLCTESNVDE.....SACCFKTHDSSSYTHLS 308

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP yvirus:*
16: SP bacteriaph:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308	100.0	308	10	Q9XFR7 arabidopsis
2	228	74.0	308	10	Q9XFR7 arabidopsis
3	171	55.5	308	10	Q9XFR7 arabidopsis
4	20	6.5	317	10	Q9XFR7 arabidopsis
5	13	4.2	354	10	Q9XFR7 arabidopsis
6	13	4.2	356	10	Q9XFR7 arabidopsis
7	13	4.2	382	10	Q9XFR7 arabidopsis
8	12	3.9	291	13	Q9XFR7 arabidopsis
9	12	3.9	291	13	Q9XFR7 arabidopsis
10	12	3.6	191	11	Q9XFR7 arabidopsis
11	11	3.6	191	11	Q9XFR7 arabidopsis
12	11	3.2	156	11	Q9XFR7 arabidopsis
13	10	3.2	156	11	Q9XFR7 arabidopsis
14	10	3.2	156	11	Q9XFR7 arabidopsis
15	10	3.2	156	11	Q9XFR7 arabidopsis
16	10	3.2	156	11	Q9XFR7 arabidopsis

17	10	3.2	355	10	Q7XAB7 euphorbia e
18	10	3.2	371	10	Q8AVB8 populus alb
19	9	2.9	153	13	P79919 xenopus lae
20	9	2.9	198	10	Q85521 zea mays (m
21	9	2.9	315	10	Q8GVBO helianthus
22	9	2.9	321	10	Q8SZFE arabidopsis
23	9	2.9	330	10	Q8SNV2 antirrhinum
24	9	2.9	349	10	Q82678 chenopodium
25	9	2.9	372	10	P93103 chenopodium
26	9	2.9	390	10	Q85522 zea mays (m
27	8	2.6	178	5	Q23641 caenorhabdi
28	8	2.6	232	17	Q97B27 thermoplas
29	8	2.6	241	2	Q9ACH9 uncultured
30	8	2.6	241	2	Q9AE50 rhizobium 1
31	8	2.6	241	2	Q9AC12 uncultured
32	8	2.6	241	2	Q9AE49 rhizobium 1
33	8	2.6	241	2	Q9AC10 uncultured
34	8	2.6	241	2	Q9AE47 rhizobium 1
35	8	2.6	241	2	Q9AC14 uncultured
36	8	2.6	241	2	Q9ACH8 uncultured
37	8	2.6	263	10	Q22156 arabidopsis
38	8	2.6	300	10	Q28718 archaeoglob
39	8	2.6	302	5	Q964G0 strongyloce
40	8	2.6	302	10	Q9ZRO4 arabidopsis
41	8	2.6	306	5	Q9NEG4 leihamania
42	8	2.6	308	10	Q81PW3 helianthus
43	8	2.6	328	16	Q9HZE3 pseudomonas
44	8	2.6	356	10	Q8LHA8 oryza sativ
45	8	2.6	357	10	Q8GVD9 helianthus

ALIGNMENTS

RESULT 1
ID Q9XFR7 PRELIMINARY; PRT; 308 AA.
AC Q9XFR7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE D-type cyclin.
GN CYCD4.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA de Veylder L., De Almeida Engler J., Bursens S., Maneyski A.,
RA Lescure B., Van Montagu M., Engler G., Inze D.;
RT "A new D-type cyclin of Arabidopsis thaliana expressed during lateral
root primordia formation."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AJ131636; CAB4347.1; -;
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin_1.
DR Pfam: PF02984; cyclin_1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34687 MW; 591ADA3361DD63D CRC64;
Query Match 100.0%; Score 308; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.7e-297; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 0;

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QY 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFSQSESEETIMENVEKEKOLPS 60
DB 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFSQSESEETIMENVEKEKOLPS 60
QY 61 DDYIKRLSGDDLNVGRDALNMWIKACEVHQFGPCLANNYLDRLFSVHDLPSGKG 120
DB 61 DDYIKRLSGDDLNVGRDALNMWIKACEVHQFGPCLANNYLDRLFSVHDLPSGKG 120
QY 121 WITQLAVACLSIAAKIEETEVPMLIDLVGDPOQFVEAKSVQRMELLVANKMLRAI 180
DB 121 WITQLAVACLSIAAKIEETEVPMLIDLVGDPOQFVEAKSVQRMELLVANKMLRAI 180
QY 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSEAAAVALSVSGE 240
DB 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSEAAAVALSVSGE 240
QY 241 LQVHFNSSPSPFLSLQKERYKIGEMIESQSDICQTPNGVLEVSACCFSEFKTHDS 300
DB 241 LQVHFNSSPSPFLSLQKERYKIGEMIESQSDICQTPNGVLEVSACCFSEFKTHDS 300
QY 301 SSSYTHLS 308
DB 301 SSSYTHLS 308

RESULT 2
ID Q9FKP7 PRELIMINARY; PRT; 308 AA.
AC Q9FKP7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE D-type cyclin.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kocant H., Nakamura Y., Sato S., Aamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:131-145(1998).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AB011479; BAB11564.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34715 MM; 96FD929C868DD62F CRC64;

Query Match 74.0%; Score 228; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 6e-218;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFSQSESEETIMENVEKEKOLPS 60
DB 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFSQSESEETIMENVEKEKOLPS 60
QY 61 DDYIKRLSGDDLNVGRDALNMWIKACEVHQFGPCLANNYLDRLFSVHDLPSGKG 120
DB 61 DDYIKRLSGDDLNVGRDALNMWIKACEVHQFGPCLANNYLDRLFSVHDLPSGKG 120

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DB 61 DDYIKRLSGDDLNVGRDALNMWIKACEVHQFGPCLANNYLDRLFSVHDLPSGKG 120
QY 121 WITQLAVACLSIAAKIEETEVPMLIDLVGDPOQFVEAKSVQRMELLVANKMLRAI 180
DB 121 WITQLAVACLSIAAKIEETEVPMLIDLVGDPOQFVEAKSVQRMELLVANKMLRAI 180
QY 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSE 228
DB 181 TPQSYIRYFLRKMSKCDQEPSNTLISRSQVIASTTKGIDPLEFRPSE 228

RESULT 3
ID Q8IGAL PRELIMINARY; PRT; 308 AA.
AC Q8IGAL;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE D-type cyclin.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldman K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldman K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RT Submitted (MAR-2002) to the EMBL/Genbank/DBS databases.
RL -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
CC EMBL; AY084386; AAM60963.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34788 MM; EB077DA1868DCC42 CRC64;

Query Match 55.5%; Score 171; DB 10; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.9e-161;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFSQSESEETIMENVEKEKOLPS 60
DB 1 MAENNELSLCTESNVDEGMIVDETPRISIPQWFSQSESEETIMENVEKEKOLPS 60
QY 61 DDYIKRLSGDDLNVGRDALNMWIKACEVHQFGPCLANNYLDRLFSVHDLPSGKG 120
DB 61 DDYIKRLSGDDLNVGRDALNMWIKACEVHQFGPCLANNYLDRLFSVHDLPSGKG 120
QY 121 WITQLAVACLSIAAKIEETEVPMLIDLVGDPOQFVEAKSVQRMELLVANKMLRAI 171
DB 121 WITQLAVACLSIAAKIEETEVPMLIDLVGDPOQFVEAKSVQRMELLVANKMLRAI 171

RESULT 4
ID Q9LX96 PRELIMINARY; PRT; 317 AA.
Q9LX96

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AC Q9LX96;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin protein-like.
GN F12B17.210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RA Bevan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: A135395; CAB89399.1; -.
DR PIR: T49995; T49995.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLIN; 1.
DR Cell cycle; Cell division; Cyclin.
KW SEQUENCE 317 AA; 35910 MW; 07616F8480927711 CRC64;
SQ
Query Match 6.5%; Score 20; DB 10; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 CLAMNYLDRFLSVHDPGSK 119
DB 91 CLAMNYLDRFLSVHDPGSK 110

RESULT 5
Q9ZRX9
ID Q9ZRX9 PRELIMINARY; PRT; 354 AA.
AC Q9ZRX9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin D2.1 protein.
GN CYCD2.1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE:9097070; PubMed:980377;
RA Sorrell D.A., Combettes B., Chaubert-Gigot N., Gigot C., Murray J.A.H.;
RT "Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels
RT of Transcripts in Tobacco Bright Yellow-2 Cells.";
RL Plant Physiol. 119:343-351(1999).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AJ011892; CA09852.1; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.

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DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 354 AA; 39714 MW; 18363A0E76E89BF CRC64;

Query Match 4.2%; Score 13; DB 10; Length 354;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLIYVACLSIAK 136
DB 142 QLIYVACLSIAK 154

RESULT 6
Q8SBC0
ID Q8SBC0 PRELIMINARY; PRT; 356 AA.
AC Q8SBC0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin.
GN OSCYCD.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipondare;
RA Nakashima M., Neogi P.B., Okano E., Hashimoto J., Sasaki T.,
RA Ichikawa H.;
RT "Nucleotide sequence of a cDNA encoding a D-type cyclin from cell
RT suspension culture of rice.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AB080248; BAB85522.1; -.
DR Gramene; Q8SBC0; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0000910; P:cytokinesis; IEA.
DR GO: GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR006670; Cyclin.
DR InterPro: IPR004367; Cyclin_Cterm.
DR InterPro: IPR006671; Cyclin_N.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 356 AA; 38937 MW; 502AF4EB9CE8BCEA CRC64;

Query Match 4.2%; Score 13; DB 10; Length 356;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLIYVACLSIAK 136
DB 149 QLIYVACLSIAK 161

RESULT 7
Q8L6U0
ID Q8L6U0 PRELIMINARY; PRT; 382 AA.
AC Q8L6U0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin D2.
GN CYCD2.
OS Daucus carota (Carrot).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulid; Apiales; Apiales; Apiales; Apiales; Apiales; Apiales;
OC Daucus.
OC NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RA Eun C.H., Ko S.W., Matsubayashi Y., Sakagami Y., Kamada H.;
RT "The effect of the peridyl growth factor, phytochrome- $\alpha$ , on
RT the cell cycle progression in carrot non-embryonic cells."
RC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CL -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AF496740; C434341.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cyclokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KM Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 382 AA; 43354 MW; 79768528D809170 CRC64;

Query Match 4.2%; Score 13; DB 10; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QILAVACLSIAK 136
DB 141 QILAVACLSIAK 153

RESULT 8
Q8AVQ4 PRELIMINARY; PRT; 291 AA.
AC Q8AVQ4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to cyclin D1 (PRAD1: parathyroid adenomatosis 1).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RC Klein S.; Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041525; AAH41525.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KM PROSITE; PS00292; CYCLINS; 1.
SQ SEQUENCE 291 AA; 33052 MW; 55316D5236F9E081 CRC64;

Query Match 3.9%; Score 12; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRLSLV 112
DB 78 LAMNYLDRLSLV 89

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RESULT 9
Q7ZYU6 PRELIMINARY; PRT; 291 AA.
AC Q7ZYU6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RC Klein S.; Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043758; AAH43758.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR PROSITE; PS00388; HLH_1; 1.
KM Hypothetical protein.
SQ SEQUENCE 291 AA; 33005 MW; 6678C2C9EACF9178 CRC64;

Query Match 3.9%; Score 12; DB 13; Length 291;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDRLSLV 112
DB 78 LAMNYLDRLSLV 89

RESULT 10
Q8QFP4 PRELIMINARY; PRT; 291 AA.
AC Q8QFP4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cyclin D1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Mature ovary;
RC Bauer M.P.; Goetz F.W.;
RL "Isolation of Cyclin D1 from the Zebrafish."
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CL -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AF365874; AA00355.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0000910; P:cyclokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR InterPro; IPR001092; HLH_basic.
SQ SEQUENCE 291 AA; 33005 MW; 6678C2C9EACF9178 CRC64;

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DR PFam: PF00134; cyclin_1.
DR PFam: PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR PROSITE; PS00038; HLH 1; 1.
DR Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 291 AA; 33080 MW; 7848FCCF2482E8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 12; DB 13; Length 291;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANVYLDRLSV 112
DB 80 LANVYLDRLSV 91

RESULT 11
ID Q99NB4 PRELIMINARY; PRT; 191 AA.
AC Q99NB4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cyclin D1 (Fragment)
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1] _TaxId=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=WiStar;
RA Morizumi A.; Ido A.; Tsubouchi H.;
RT "Characterization of rat cyclin D1 5' flanking region.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AB042564; BAB4033.1; -.
DR HSSP; P30274; IVIN.
DR GO; GO:0005634; Cytocinesis; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR PROSITE; PS00038; HLH 1; 1.
DR Cell cycle; Cell division; Cyclin.
KW NON TER
SQ SEQUENCE 191 AA; 22203 MW; AA97B60F332EDEE CRC64;

Query Match
Best Local Similarity 100.0%; Score 11; DB 11; Length 191;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LANVYLDRLSV 111
DB 80 LANVYLDRLSV 90

RESULT 12
ID Q88524 PRELIMINARY; PRT; 358 AA.
AC Q88524;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE D-type cyclin.
GN CYCD2.
OS Zea mays (Maize).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACMAD clade; Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxId=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Mo17;
RA Tao Y.; Lowe K.; Gregory C.; Coughlan S.J.; Gordon-Kamm W.J.;
RT "Isolation of a family of D-type cyclins from maize that show
RT conserved and unique characteristics.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AF351189; BAB3926.1; -.
DR GO; GO:0005634; Cytocinesis; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR PROSITE; PS00038; HLH 1; 1.
DR Cell cycle; Cell division; Cyclin.
KW SEQUENCE 358 AA; 38836 MW; D25B39B7D640837 CRC64;

Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 358;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 QLLAVACSLA 134
DB 148 QLLAVACSLA 158

RESULT 13
ID Q9DBL9 PRELIMINARY; PRT; 156 AA.
AC Q9DBL9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cyclin D2.
GN CCND2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J.; Shinagawa A.; Shibata K.; Yoshino M.; Itoh M.; Ishii Y.;
RA Arakawa T.; Hara A.; Fukunishi Y.; Kono H.; Adachi S.; Yamakata I.;
RA Aizawa K.; Izawa M.; Niehi K.; Kiyosawa H.; Kondo J.; Yamakata I.;
RA Saio T.; Okazaki Y.; Gojobori T.; Bono H.; Kasukawa T.; Saio R.;
RA Kadoya K.; Macera H.A.; Ashburner M.; Batalov S.; Caavaant T.;
RA Fleischmann W.; Gaasterland T.; Gissi C.; King B.; Kochiwa H.;
RA Kuehl P.; Lewis S.; Matsuo Y.; Nikaide I.; Pesole G.; Quackenbush J.;
RA Schriml L.M.; Staubli F.; Suzuki R.; Tomita M.; Wagner L.; Mashio T.;
RA Sakai K.; Okido T.; Furuno M.; Aono H.; Baldarelli R.; Barsh G.;
RA Blake J.; Boffelli D.; Bojunga N.; Carninci P.; de Bonaldo M.F.;
RA Brownstein M.C.; Bult C.; Fletcher C.; Fujita M.; Gariboldi M.;
RA Gustinich S.; Hill D.; Hofmann M.; Hume D.A.; Kamuya M.; Lee N.H.;
RA Lyons P.; Marchionni L.; Mashima J.; Mazzarelli J.; Mombaerts P.;
RA Nordone P.; Ring B.; Ringwald M.; Rodriguez I.; Sakamoto N.;
RA Sasaki H.; Sato K.; Schoenbach C.; Seya T.; Shibata Y.; Storch K.-F.;
RA Suzuki H.; Toyokawa K.; Wang K.H.; Weltz C.; Whitaker C.; Wilming L.;
RA Wyszynski B.; Yoshida K.; Hasegawa Y.; Kawai H.; Kohseki S.;
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

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DR EMBL; AJ007904; BAB25338.1; --
 DR HSSP; P35274; 1VIN.
 DR GGD; MG188314; Concl2.
 DR GO; GO:0000074; P:regulation of cell cycle; IMP.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin_1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 DR Cell cycle; Cell division; Cyclin.
 KW SEQUENCE 156 AA; 18080 MW; C0215E724C6B9CFE CRC64;
 SQ

Query Match 3.2%; Score 10; DB 11; Length 156;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDREFL 110
 DB 78 LAMNYLDREFL 87

RESULT 14
 ID 057481 PRELIMINARY; PRT; 190 AA.
 AC 057481;
 DT 01-JUN-1998 (TRENBLREL. 06, Created)
 DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Cyclin D (Fragment).
 OS Stizostedion vitreum.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
 OC Percidae; Stizostedion.
 OC NCBI_TaxID=57868;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98440539; PubMed=9765420;
 RA Lapiere L.A., Casey J.W., Holtschu D.L.;
 RT "Walleys retroviruses associated with skin tumors and hyperplasias
 RT encode cyclin D homologs.";
 RL J. Virol. 72:8765-8771(1998).
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
 DR EMBL; AF037570; AAC68476.1; --
 DR HSSP; P30274; 1VIN.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0000910; P:cytokinesis; IEA.
 DR GO; GO:0000074; P:regulation of cell cycle; IEA.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin_1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR Cell cycle; Cell division; Cyclin.
 KW NON TER 1
 FT NON TER 1
 SQ SEQUENCE 190 AA; 21445 MW; 5EB1B9BA969C01BC CRC64;
 SQ

Query Match 3.2%; Score 10; DB 13; Length 190;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 LAMNYLDREFL 110
 DB 18 LAMNYLDREFL 27

RESULT 15
 ID 09SNV1 PRELIMINARY; PRT; 343 AA.
 AC 09SNV1;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)

DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Cyclin D3a (Fragment).
 GN CYC3A.
 OS Antirrhinum majus (Garden snapdragon).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
 OC NCBI_TaxID=4151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gaudin V., Lunnese P., Fobert P., Towers M., Riou-Khamlich C.,
 RA Murray J., Coen E., Doonan J.H.;
 RT "The expression of D-cyclin genes define distinct developmental zones
 RT in Antirrhinum apical meristems and is locally regulated by the
 RT cycloidea gene.";
 RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
 DR EMBL; AJ250397; CAB61222.1; --
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0000910; P:cytokinesis; IEA.
 DR GO; GO:0000074; P:regulation of cell cycle; IEA.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR InterPro; IPR006671; Cyclin_N.
 DR Pfam; PF00134; cyclin_1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLIN; 1.
 DR Cell cycle; Cell division; Cyclin.
 KW NON TER 343
 FT NON TER 343
 SQ SEQUENCE 343 AA; 39254 MW; 128210AB2FC6E2C6 CRC64;
 SQ

Query Match 3.2%; Score 10; DB 10; Length 343;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 AVACLSIAAK 136
 DB 136 AVACLSIAAK 145

Search completed: March 23, 2004, 16:48:14
 Job time : 65 secs